SEQUENCE LISTING

<110>	University of Utah Research Foundation Cognetix, Inc. Olivera, Baldomero M. McIntosh, J. Michael Watkins, Maren Garrett, James E. Shon, Ki-Joon Jacobsen, Richard Jones, Robert M. Cartier, G. Edward	
<120>	Omega-Conopeptides	
<130>	2314-241	
<150> <151>	US 60/219,616 2000-07-21	
<150> <151>	US 60/265,888 2001-02-05	
<160>	413	
<170>	PatentIn version 3.0	
<210>	1	
<21 1> <212>	318 DNA	
<213>	Unknown	
<220> <223>	unknown Conus species	
<400>	1	
	atga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa	60
	acag ctgatgactc cagaggtacg cagaagcatc atgccctgag gtcgaccacc	120
	cca cgttgactcg tcgctgcctt tctcccggat cacgatgtca taagacaatg	180
	gct gcacttcatg ctcttcatac aaagggaaat gtcggcctcg aaaatgaacc	240
actcatc	acc tactcctctg gaggcctcag aggaattaca ttgaaataaa agccgcatta	300
caaaaaa	aaa aaaaaaa	318
<211> <212>	2 76 PRT Unknown	
<220> <223>	unknown Conus species	
	2	
	Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala 5 10 15	
	Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His 20 25 30	
Ala Leu	Arg Ser Thr Thr Asn Phe Ser Thr Leu Thr Arg Arg Cys Leu 45	

```
Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys Thr Ser
Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys
                    70
<210>
<211>
       30
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<220>
<221>
       PEPTIDE
<222>
      (1)..(30)
<223>
       Xaa at residue 4 and 28 is Pro or Hyp; Xaa at residue 22 is Tyr,
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
<400>
Cys Leu Ser Xaa Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
Thr Ser Cys Ser Ser Xaa Lys Gly Lys Cys Arg Xaa Arg Lys
<210> 4
<211> 283
<212> DNA
<213> Unknown
<220>
<223> unknown Conus species
<400>
ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggtctgtcaa
                                                                      60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc atgccctgag gtcgaccacc
                                                                     120
aattteteea egtegaeteg tegetgeaaa eeteeeggaa gaaaatgtet gaatagaaag
                                                                     180
aatgaatgct gcagcaagtt ttgcaatgaa cacctacata tgtgtggata aatggctaaa
                                                                     240
aactgaataa aagccgcatt gcaaaaaaaa aaaaaaaaa aaa
                                                                     283
<210>
<211> 74
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<400> 5
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Val
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His
Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Ser Thr Arg Arg Cys Lys
                            40
```

```
Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys Ser Lys
                        55
Phe Cys Asn Glu His Leu His Met Cys Gly
<210>
<211> 27
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<220>
<221> PEPTIDE
<222>
       (1)..(27)
<223> Xaa at residue 14 and 22 is Glu or gamma-carboxy Glu; Xaa at resi
       due 3 and 4 is Pro or Hy
<400> 6
Cys Lys Xaa Xaa Gly Arg Lys Cys Leu Asn Arg Lys Asn Xaa Cys Cys
Ser Lys Phe Cys Asn Xaa His Leu His Met Cys
            20
<210>
<211>
       275
<212>
      DNA
<213> Unknown
<220>
<223> unknown Conus species
<400> 7
ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa
                                                                      60
ctcgtcacag ctgatggctc cagaggtatg cagaagcatt atgccctgag gtcgaccacc
                                                                     120
aatototoca tatogtotog otgoaaacot occagaagaa aatgtotgaa gattaaqqat
                                                                     180
aaatgctgca acttttgcaa tacacaccta aatatgtgtg gataaatggc taaaaactga
                                                                     240
ataaaagccg cattgcaaaa aaaaaaaaaa aaaaa
                                                                     275
<210>
      72
<211>
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<400> 8
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met Gln Lys His Tyr
Ala Leu Arg Ser Thr Thr Asn Leu Ser Ile Ser Ser Arg Cys Lys Pro
        35
                                                45
```

```
Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys Asn Phe Cys
Asn Thr His Leu Asn Met Cys Gly
<210>
      9
<211>
      26
<212>
      PRT
<213> Unknown
<220>
<223> unknown Conus species
<220>
<221>
      PEPTIDE
<222>
       (1)..(26)
<223> Xaa at residue 3 and 4 is Pro or Hyp
<400> 9
Cys Lys Xaa Xaa Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys
                5
Asn Phe Cys Asn Thr His Leu Asn Met Cys
<210>
      10
       377
<211>
<212>
      DNA
<213> Unknown
<220>
<223> unknown Conus species
<400> 10
qqatccatqa aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgat ggcctgtcaa
                                                                      60
ctcqtcacag ctgatgqctc cagaggtatg cacaagcatt atgccctgag gtcgaccacc
                                                                     120
aaactctcca tgtcgactcg ctgcgcaggt ccaggaacaa tttgtcctaa tagggtatgc
                                                                     180
                                                                     240
tgcggttatt gcagtaaaag aacacatcta tgtcattcgc gaactggctg atcttccccc
ttctqcqctc catccttttc tqcctqaqtc ctccatacct gagaatggtc atgaaccact
                                                                     300
                                                                     360
caacacctac teetetqqaq qgeeteagaa qagetacatt gaaataaaag cegeattaca
aaaaaaaaa aaaaaaa
                                                                     377
<210> 11
<211>
      74
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<400> 11
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Met Ala
Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met His Lys His Tyr
                                25
Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Ser Thr Arg Cys Ala Gly
```

	35					40					45				
Pro Gly	y Thr	Ile	Cys	Pro	Asn 55	Arg	Val	Cys	Cys	Gly 60	Tyr	Cys	Ser	Lys	
Arg Th:	r His	Leu	Cys	His 70	Ser	Arg	Thr	Gly							
<210> <211> <212> <213>	12 28 PRT Unkno	own													
<220> <223>	unkn	own (Conu	s spe	ecies	5									
<220> <221> <222> <223>		.(28) at re	esid											16 is O-phos	
<400> Cys Ala	12 a Gly	Xaa	Gly 5	Thr	Ile	Cys	Xaa	Asn 10	Arg	Val	Cys	Cys	Gly 15	Xaa	
Cys Se	r Lys	Arg 20	Thr	His	Leu	Cys	His 25	Ser	Arg	Thr					
<210> <211> <212> <213>	13 323 DNA Conu	s are	enatı	ıs											
<400> ggatcca	13 atga a	aact	gacg	tg ca	atggi	igato	c ato	cgcc	gtgc	tgtt	cat	gac (ggcct	tgtcaa	60
ctcatta	acag (gtga	gcaga	aa g	gacca	atgct	t ct	gaggt	caa	ctga	acaa	aaa (ctcca	aagttg	120
actagge	cagt o	gata	ggcta	aa c	ggtg	gatct	t tgt	tacto	cgtc	attt	tca	ctg (ctgca	agcctc	180
tattgca	aata a	aagat	ttcca	ag to	gtate	gtgt	g gca	aacct	cat	acco	cgtga	agt (ggcca	atgaac	240
ccctca	atac o	cata	tcct	ct g	gaggo	cttca	a gaq	ggaad	ctgc	atte	gaaat	taa a	aacc	gcattg	300
caataa	aaaa a	aaaa	aaaa	aa aa	aa										323
<210> <211> <212> <213>	14 73 PRT Conu	s are	enatı	ıs											
<400> Met Lys 1	14 s Leu	Thr	Cys 5	Met	Val	Ile	Ile	Ala 10	Val	Leu	Phe	Leu	Thr 15	Ala	
Cys Gli	n Leu	Ile 20	Thr	Gly	Glu	Gln	Lys 25	Asp	His	Ala	Leu	Arg 30	Ser	Thr	
Asp Lys	s Asn 35	Ser	Lys	Leu	Thr	Arg 40	Gln	Cys	Ser	Ala	Asn 45	Gly	Gly	Ser	
Cys Tha	r Arg	His	Phe	His	Cys 55	Cys	Ser	Leu	Tyr	Cys 60	Asn	Lys	Asp	Ser	

```
Ser Val Cys Val Ala Thr Ser Tyr Pro
65
<210> 15
<211>
      PRT
<212>
<213>
      Conus arenatus
<220>
<221>
      PEPTIDE
       (1)..(33)
<222>
      Xaa at residue 1 is Gn or pyro-Glu; Xaa at residue 33 is Pro or H
<223>
       yp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 15
Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
Xaa
<210>
       16
<211>
       326
<212>
       DNA
      Conus arenatus
<213>
<400> 16
accaaaacca tcatcaaaat gaaactgacg tgcgtgttga ttatcgccgt gctgttcctg
                                                                       60
acqqcctqtc aactcattac aqctqaqact tactccagag gtgagcagaa gcaccatgct
                                                                      120
ctgaggtcaa ctgacagaaa ctccaagttg accaggacat gcaacactcc cactgaatat
                                                                      180
                                                                      240
tqtactttqc atcgacactg ctgcagcggc tactgccata aaacaatcca ggcatgttca
taataccggt gagtggtcat gaaccactca ataccctctc ctctggaggc ttcagaggaa
                                                                      300
                                                                      326
ctgcattgaa ataaaagccg cattgc
<210> 17
<211>
      74
<212> PRT
<213> Conus arenatus
<400> 17
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His
His Ala Leu Arg Ser Thr Asp Arg Asn Ser Lys Leu Thr Arg Thr Cys
Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys Ser Gly
Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
                     70
```

```
<210>
       18
<211>
       28
<212>
       PRT
       Conus arenatus
<213>
<220>
<221>
       PEPTIDE
<222>
       (1)..(28)
       Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is
<223>
        Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-
       Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 18
Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Arg His Cys Cys
Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
<210>
       19
<211>
       332
<212>
       DNA
<213>
      Conus arenatus
<400> 19
accaaaacca tcatcaaaat gaaactgacg tgcgtgttga tcatcgccgt gctgttcctg
                                                                        60
acggcctgtc aactcattac agctgagact tactccagag gtgagcagat gcaccgtgct
                                                                       120
ctgaggtcaa ctgacaaaaa ctccaagttg actaggcagt gcacgcctaa cggtggatct
                                                                       180
tgttctcgtc attttcactg ctgcagcctc tattgcaata aaagtactgg cgtatgtatt
                                                                       240
gcaacctcat accegtgagt ggtcatgaac cactcaatac ceteteetet ggaggettca
                                                                       300
                                                                       332
gaggaactgc attgaaataa aagccgcatt gc
<210>
       20
<211>
       79
<212>
       PRT
<213> Conus arenatus
<400> 20
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Met His
Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
 Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
 Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr Pro
 <210>
        21
 <211>
        33
 <212>
        PRT
 <213>
        Conus arenatus
 <220>
 <221> PEPTIDE
```

<222> (1)..(33)Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 33 is P <223> ro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-T yr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty Xaa Cys Thr Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu Xaa Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Xaa Xaa <210> 22 <211> 332 DNA <212> <213> Conus arenatus <400> 22 ggatccatga aactgacgtg catggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60 ctcattacag ctgagactta ctccagaggt gagcagaagc accatgctct gaggtcaact 120 gacaaaaact ccaagttgac caggacatgc aacactccca ccgaatattg tactttgcat 180 240 caacactgct gcagcggcta ctgccataaa acaatccagg catgttcata ataccggtga gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300 332 aaaaccqcat tacaaaaaaa aaaaaaaaaa aa <210> 23 <211> 74 <212> PRT <213> Conus arenatus <400> 23 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His His Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly Tyr Cys His Lys Thr Ile Gln Ala Cys Ser <210> 24 <211> 28 <212> PRT <213> Conus arenatus <220> <221> PEPTIDE <222> (1)..(28)Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-

Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

```
<400> 24
Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys
Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
<210>
       25
<211>
       394
<212>
       DNA
<213>
      Conus arenatus
<400> 25
ggatccatga aactgacgtg tatggtgatc atcgccgtac tgttcctgac ggcctgtcaa
                                                                      60
ctcattacag ctgagactta ctccagaggt aagcagatgc accgcgctct gaggtcaact
                                                                      120
                                                                      180
qacaaaaact cccagttgac cagggaatgc acacctcccg gtggagcttg tggtttacct
acacactgct gcgggttttg cgatactgca aacaacagat gtctgtaaag ctggtctqqc
                                                                      240
gtctgatatt ccccttctgt gctctatcct ctttggcctg agtcatccgt acctgtgagt
                                                                      300
ggtcatgaac tactcaatac cctctcctct ggaggcttca gaggaactac aatgaaataa
                                                                      360
                                                                      394
aacccqcatt gcagagaaaa aaaaaaaaaa aaaa
       26
<210>
      73
<211>
<212> PRT
<213> Conus arenatus
<400> 26
Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
Cys Asp Thr Ala Asn Asn Arg Cys Leu
<210> 27
<211>
       27
<212> PRT
<213> Conus arenatus
<220>
<221> PEPTIDE
<222>
       (1)..(27)
       Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5
        and 12 is Pro or Hy
<400> 27
Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
```

Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu

25 20 <210> 28 345 <211> <212> DNA <213> Conus arenatus <220> <221> misc_feature <222> (1)..(345) <223> n may be any nucldeotide <400> 28 ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60 ctcattacag ctgagactta ctccagaggt gagcagaatc accatgttct gaggtcaact 120 qacaaaaact ccaagttgac caggacatgc aacactccca ctgaatattg tactttgcat 180 caacactgct gcagcggcca ctgccataaa acaatccagg catgtgcata ataccggtgg 240 300 gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 345 aaaaccgcat tgcaatgaan aaaaaaaaaa aaaaaaaaa aaaaa <210> 29 <211> 74 <212> PRT <213> Conus arenatus <400> 29 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Asn His His Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala <210> 30 <211> 28 <212> PRT <213> Conus arenatus <220> <221> PEPTIDE <222> (1)..(28)Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di -iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty <400> 30 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala

```
31
<210>
<211>
       322
<212>
       DNA
      Conus arenatus
<400> 31
ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctgac ggcctgtcaa
                                                                       60
ctcactacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg
                                                                       120
actaggcagt getegeetat eggtggatat tgtactette atatteactg etgeageaac
                                                                       180
cattgcatta aacctatcgg ccgatgtgtg gcaacctgat acccgtgcgt ggtcatgaac
                                                                       240
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg
                                                                       300
caataaaaaa aaaaaaaaaa aa
                                                                      322
<210>
       32
      70
<211>
<212>
      PRT
<213>
      Conus arenatus
<400> 32
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Pro Ile Gly Gly Tyr
Cys Thr Leu His Ile His Cys Cys Ser Asn His Cys Ile Lys Pro Ile
Gly Arg Cys Val Ala Thr
<210>
       33
<211>
       30
<212>
       PRT
<213>
       Conus arenatus
<220>
<221>
      PEPTIDE
<222>
       (1)..(30)
<223>
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P
       ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i
       odo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 33
Xaa Cys Ser Xaa Ile Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys
Ser Asn His Cys Ile Lys Xaa Ile Gly Arg Cys Val Ala Thr
                                 25
       34
<210>
<211>
       318
<212>
       DNA
<213>
      Conus arenatus
<400> 34
ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac ggcctgtcaa
                                                                       60
```

ctcactacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg	120					
actaggcagt gcttgcctaa cggtggatat tgtactcttc atattcactg ctgcagcgac	180					
cattgcatta aacctatcga ccgatgtgtg gcaacctgat acccgggcgt ggtcatgaac	240					
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta	300					
Caaaaaaaaa aaaaaaaa	318					
<210> 35 <211> 70 <212> PRT <213> Conus arenatus						
<pre><400> 35 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala 1</pre>						
Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr 20 25 30						
Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Leu Pro Asn Gly Gly Tyr 35 40 45						
Cys Thr Leu His Ile His Cys Cys Ser Asp His Cys Ile Lys Pro Ile 50 55 60						
Asp Arg Cys Val Ala Thr 65 70						
<210> 36 <211> 30 <212> PRT <213> Conus arenatus						
<pre><220> <221> PEPTIDE <222> (1)(30) <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i odo-Tyr, O-sulpho-Tyr or O-phospho-Ty</pre>						
<400> 36 Xaa Cys Leu Xaa Asn Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys 1 5 10 15						
Ser Asp His Cys Ile Lys Xaa Ile Asp Arg Cys Val Ala Thr 20 25 30						
<210> 37 <211> 374 <212> DNA <213> Conus aurisiacus						
<400> 37 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc	60					
acagetgatg actecagagg taegeagaag categtteee tgagetegge caecaaacte	120					
tccatgtcga ctcgctgcaa gggtaaagga aaaccatgca gtaggatttc gtataactgc	180					

tgcaccggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgatc ttcccccttc 240

tgtgctctat ccttttctgc ctgagtcctc cttacctgag agtggtcatg aaccactcat 300
cacctgctcc tctggaggcc ccagaggagc tacattgaaa taaaagtcgc attgcaaaaa 360
aaaaaaaaa aaaa 374
<210> 38 <211> 71 <212> PRT <213> Conus aurisiacus
<400> 38 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala 1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg 20 25 30
Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly 35 40 45
Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys Thr Gly Ser 50 55 60
Cys Arg Ser Gly Lys Cys Gly 65 70
<210> 39 <211> 25 <212> PRT <213> Conus aurisiacus
<220> <221> PEPTIDE <222> (1)(25) <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 39 Cys Lys Gly Lys Gly Lys Xaa Cys Ser Arg Ile Ser Xaa Asn Cys Cys 1 5 10 15
Thr Gly Ser Cys Arg Ser Gly Lys Cys 20 25
<210> 40 <211> 380 <212> DNA <213> Conus aurisiacus
<400> 40 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60
acagetgatg actecagagg taegeagaag categtteee tgaggtegaa gaccaaacte 120
tocatgtoga otggotgoat ggaagoogga tottattgog gototactao gagaatotgo 180
tgcggttttt gcgcttattt cggcaaaaaa tgtattgact atcccagcaa ctgatcttcc 240
ccctactgtg ctctatcctt ttctgcctga gtcctcctta cctgagagtg gtcatgaacc 300
actcatcacc tgctcctctg gaggccccag aggagctaca ttgaaataaa atcgcattgc 360
taaaaaaaaa aaaaaaaaaa 380

```
<210>
      41
       77
<211>
<212>
       PRT
<213> Conus aurisiacus
<400> 41
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu
Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys Gly Phe Cys
Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
                    70
<210>
       42
<211>
<212>
       PRT
<213>
       Conus aurisiacus
<220>
<221>
      PEPTIDE
<222>
       (1)..(32)
<223>
      Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 30 i
       s Pro or Hyp; Xaa at residue 7, 21 and 29 is Tyr, 125I-Tyr, mono-
       iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 42
Cys Met Xaa Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg Ile Cys Cys
Gly Phe Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa Xaa Ser Asn
<210>
      43
<211>
       373
<212>
       DNA
<213>
       Conus aurisiacus
<400> 43
accaaaacca tcatcaaaat qaaactqacq tqtqtqqtqa tcqtcqccqt qctqctcctq
                                                                       60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg
                                                                      120
ageteggeea ceaaactete catgtegaet egetgeaagg etaaaggaaa accatgeagt
                                                                      180
aggattgcgt ataactgctg caccggttct tgcagatcag gtaaatgtgg ctgatccagt
                                                                      240
gcctgatctt cccccttctg tgctctatcc ttttctgcct gagtcctcct tacctgagag
                                                                      300
tggtcatgaa ccactcatca cctgctcctc tggaggcccc agaggagcta cattgaaata
                                                                      360
aaagccgcat tgc
                                                                      373
<210>
      44
<211>
       71
<212>
      PRT
<213> Conus aurisiacus
```

```
<400> 44
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
Cys Arg Ser Gly Lys Cys Gly
<210>
      45
<211>
       25
<212> PRT
<213> Conus aurisiacus
<220>
<221>
      PEPTIDE
       (1)..(25)
<222>
      Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
<223>
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 45
Cys Lys Ala Lys Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
            20
<210>
       46
       379
<211>
<212>
       DNA
<213>
      Conus aurisiacus
<400> 46
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctqctcctq
                                                                       60
acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg
                                                                      120
aggtcgaaga caaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt
                                                                      180
                                                                      240
qqtattqaca acqactgctg caatgcatgc gatccaggaa gaaatatatg tacgtagctg
atccagogoc tgatottoco cottotgtgo totatocttt totgocogag tootoottac
                                                                      300
                                                                      360
ctgagagtgg tcatgaacca ctcatcacct gctccctgga ggcctcagag gagctacaat
                                                                      379
gaaataaaag ccgcattgc
      47
<210>
<211>
       72
<212>
       PRT
<213>
       Conus aurisiacus
<400> 47
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Thr
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
            20
```

```
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
                            40
        35
Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
Asp Pro Gly Arg Asn Ile Cys Thr
<210>
       48
<211>
       26
<212>
       PRT
<213> Conus aurisiacus
<220>
<221>
       PEPTIDE
<222>
       (1)..(26)
       Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
<223>
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 48
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
Ala Cys Asp Xaa Gly Arg Asn Ile Cys Thr
       49
<210>
<211>
       382
<212>
       DNA
<213>
       Conus bullatus
<400> 49
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg
                                                                       60
acggcctgtc agctcattac agctgaagac tccagaggta cgcatgagca tcttgccctg
                                                                       120
                                                                       180
aaqtcqacct ccaaaqtctc caagtcgact agctgcatgg aagccggatc ttattgcgga
                                                                       240
cctqctacta cqaaaatctq ctqcqatttt tqcaqtccat tcaqcqataq atgtatqaac
                                                                       300
aatcccaaca attgatcttc ccccttgtgt gctccatcct tttctgcctg agtcctcctt
acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac
                                                                       360
attgaaataa aagccgcatt gc
                                                                       382
       50
<210>
       78
<211>
<212>
       PRT
<213> Conus bullatus
<400> 50
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
```

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe

50	55	60
Cys Ser Pro Phe Ser Asp 65 70	Arg Cys Met Asn Asn 75	Pro Asn Asn
<210> 51 <211> 36 <212> PRT <213> Conus bullatus		
25 and 34 is Pro	is Glu or gamma-cark or Hyp; Xaa at resid do-Tyr, O-sulpho-Tyr	poxy Glu; Xaa at residue 13, due10 is Tyr, 125I-Tyr, mono or O-phospho-Ty
<400> 51 Ser Thr Ser Cys Met Xaa 1 5	Ala Gly Ser Xaa Cys 10	Gly Xaa Ala Thr Thr 15
Lys Ile Cys Cys Asp Phe	Cys Ser Xaa Phe Ser 25	Asp Arg Cys Met Asn 30
Asn Xaa Asn Asn 35		
<210> 52 <211> 400 <212> DNA <213> Conus bullatus		
<400> 52 accaaaacca tcatcaaaat g	aaactgacg tgtgtggtga	tegtegeegt getgeteetg 60
acggcctgtc agctcattac a		
aggaaggcca ccaaacaccc t	gtgtcgact cgctgcatta	ctccaggaac acgatgtaag 180
gttccgagcc aatgctgcag a	ggtccttgc aagaacggtc.	gttgtactcc atccccttct 240
gaatggtaaa tgtggttgat o	cagegeetg atetteecee	ttcgtcgtgc tccatccttt 300
tctgcctgag tcctccttac (tgagagtgg tcatgaacca	ctcatcacct actcccctgg 360
aggetteaga ggagetaeat t	gaaataaaa gccgcattgc:	400
<210> 53 <211> 76 <212> PRT <213> Conus bullatus		
<400> 53 Met Lys Leu Thr Cys Val 1 5	l Val Ile Val Ala Val 10	Leu Leu Thr Ala 15
Cys Gln Leu Ile Thr Ala 20	a Glu Asp Ser Arg Gly 25	Thr Gln Leu His Arg 30
Ala Leu Arg Lys Ala Th:	r Lys His Pro Val Ser 40	Thr Arg Cys Ile Thr 45
Pro Gly Thr Arg Cys Ly:	s Val Pro Ser Gln Cys 55	Cys Arg Gly Pro Cys 60

```
Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp
                    70
<210>
       54
<211>
      31
<212>
      PRT
<213> Conus bullatus
<220>
<221>
      PEPTIDE
<222>
       (1)..(31)
       Xaa at residue 30 is Glu or gamma-carboxy Glu; Xaa at residue 4,
<223>
       11, 18, 26 and 28 is Pro or Hyp; Xaa at residue 31is Trp or Bromo
<400> 54
Cys Ile Thr Xaa Gly Thr Ala Cys Lys Val Xaa Ser Gln Cys Cys Arg
Gly Xaa Cys Lys Asn Gly Arg Cys Thr Xaa Ser Xaa Ser Xaa Xaa
<210>
<211>
      379
<212> DNA
<213> Conus bullatus
<400> 55
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg
                                                                       60
                                                                      120
acggcctgtc agctcattac agctgaggac tccagagata cgcagaagca tcgtgccctg
aggtcggaca ccaaactctc catgttgact ttgcgctgcg caacttacgg aaaaccttgt
                                                                      180
                                                                      240
ggtattcaaa acqactqctq caatacatgc gatccagcca gaaggacatg tacgtagctg
atccggcgtc ttgatcctcc gcttctgtgc tccatctttt ctgcctgagt cctccttacc
                                                                      300
                                                                      360
tqaqaqtqqt catqaaccac tcatcaccta ctcctctgga ggctttagag gagctacatt
                                                                      379
gaaataaaag ccgcattgc
<210>
       56
<211>
       72
<212>
       PRT
<213>
       Conus bullatus
<400> 56
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Asp Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn Thr Cys
Asp Pro Ala Arg Arg Thr Cys Thr
<210>
       57
<211>
       26
```

```
<212> PRT
<213> Conus bullatus
<220>
<221> PEPTIDE
<222>
      (1)..(26)
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 57
Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
Thr Cys Asp Xaa Ala Arg Arg Thr Cys Thr
            20
<210> 58
<211>
       373
<212>
       DNA
<213>
      Conus bullatus
<400> 58
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg
                                                                      60
acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg
                                                                      120
                                                                      180
aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc atcatgtata
aggattgcgt ataactgctg caagtattct tgcagaaatg gtaaatgtgg ctgatccagc
                                                                      240
gcctgatctt cccccttgtg tgctccatcc ttttctgcct gagtcctcct tacctgagag
                                                                      300
tggtcatgaa ccactcatca cctactcctc tggaggcttc agaggagcta cattgaaata
                                                                      360
                                                                      373
aaagccqcat tqc
<210> 59
<211>
      71
<212> PRT
<213> Conus bullatus
<400> 59
Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
                                             60
Cys Arg Asn Gly Lys Cys Gly
65
       60
<210>
<211>
       25
       PRT
<212>
<213> Conus bullatus
<220>
<221> PEPTIDE
```

```
<222>
      (1)..(25)
      Xaa at residue 4 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,
<223>
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
<400>
       60
Cys Lys Gly Xaa Gly Ala Ser Cys Ile Arg Ile Ala Xaa Asn Cys Cys
Lys Xaa Ser Cys Arg Asn Gly Lys Cys
<210>
       61
<211>
      382
<212>
      DNA
<213>
      Conus bullatus
<400> 61
atcaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                       60
acggcctgtc agctcattac agctgaagac tccagaggta cgcatgagca tcttgccctg
                                                                      120
aaqtcqacct ccaaaqtctc caagtcgact agctgcatgg cagccggatc ttattgcgga
                                                                      180
cctgctacta cgaatatctg ctgcgatttt tgcagtccat tcagcgatag atgtatgaaa
                                                                      240
aagcccaaca attgatcttc ccccttctgt gctctatcct tttctgcctg agtcctcctt
                                                                      300
acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac
                                                                      360
attgaaataa aagccgcatt gc
                                                                      382
<210>
       62
<211>
       78
<212>
       PRT
<213> Conus bullatus
<400> 62
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala
Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Asn Ile Cys Cys Asp Phe
Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn
                    70
                                        75
<210>
       63
<211>
       36
<212>
       PRT
<213>
      Conus bullatus
<220>
<221>
       PEPTIDE
<222>
      (1)...(36)
<223>
      Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is
       Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
       pho-Ty
```

```
<400> 63
Ser Thr Ser Cys Met Ala Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
Asn Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Lys
Lys Xaa Asn Asn
        35
<210>
      64
       373
<211>
<212>
      DNA
      Conus bullatus
<213>
<400> 64
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                      60
                                                                     120
acqqcctqtc agctcattat agctgaggac tccagaggta cgcagttgca tcgtgccctg
aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtaaaggatc atcatgtcat
                                                                      180
                                                                      240
aggacttcgt atgactgctg cacgggttct tgcagaaatg gtagatgtgg ctgatccagc
gcctgatctt cccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag
                                                                      300
                                                                      360
tggtcatgaa ccactcatca cctactcctc tggaggcttc agaggagcta cattgaaata
                                                                      373
aaagccgcat tgc
<210> 65
      71
<211>
<212> PRT
<213> Conus bullatus
<400> 65
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Ile Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
Cys Arg Asn Gly Arg Cys Gly
<210> 66
<211>
      25
<212> PRT
<213> Conus bullatus
<220>
<221>
       PEPTIDE
       (1)..(25)
<222>
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 66
Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
```

```
Thr Gly Ser Cys Arg Asn Gly Arg Cys
<210>
       67
<211>
      321
<212>
      DNA
      Conus caracteristicus
<213>
<400>
ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac ggcctgtcaa
                                                                       60
ctcattacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg
                                                                      120
actaggcagt gctcggctaa cggtggatct tgtactcgtc attttcactg ctgcagcctc
                                                                      180
tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac
                                                                      240
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta
                                                                      300
                                                                      321
caaaaaaaa aaaaaaaaaa a
<210>
       68
<211>
       73
      PRT
<212>
      Conus caracteristicus
<213>
<400>
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser
                         55
Ser Val Cys Val Ala Thr Ser Tyr Pro
<210>
       69
       33
<211>
<212>
      PRT
<213> Conus caracteristicus
<220>
<221>
       PEPTIDE
<222>
       (1)..(33)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 33 is Pro or
<223>
       Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di
       -iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 69
Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
```

Xaa

```
<210>
      70
      26
<211>
      PRT
<212>
<213> Conus catus
<400> 70
Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
Thr Gly Ser Cys Arg Ser Gly Arg Cys Gly
<210>
       71
<211>
       25
<212>
      PRT
<213>
      Conus catus
<220>
<221>
      PEPTIDE
<222>
       (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 71
Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
Thr Gly Ser Cys Arg Ser Gly Arg Cys
       72
<210>
<211>
       229
<212>
       DNA
<213> Conus catus
<400> 72
tcgactcgct gccagggtag aggagcatca tgtcgtaaga ctatgtataa ctgctgcagc
                                                                       60
ggttcttgca acagaggtag ttgtggctga tccggcgcct gatcttcccc cttccgtgct
                                                                      120
ctatectttt etgeetgatt eeteettaee tgagageggt catgaaceae teateaeetg
                                                                       180
                                                                       229
ctcctctgga ggcctcagag gagctacatt gaaataaaag ccgcattgc
<210>
       73
<211>
       29
<212>
       PRT
<213>
       Conus catus
<400> 73
Ser Thr Arg Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr
Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys Gly
<210>
       74
<211>
       25
<212>
       PRT
<213>
       Conus catus
<220>
       PEPTIDE
<221>
       (1)..(25)
<222>
<223>
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
```

-sulpho-Tyr or O-phospho-Ty

<400> 74 Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys 75 <210> <211> 235 <212> DNA <213> Conus catus <400> 75 tcgacacgct gcttgcctgc cggagagtct tgccttttta gtaggattag atgctgcggt 60 acttgcagtt cagtcttaaa gtcatgtgtg agctgatcca gctgctgatc ttcctcctcc 120 tgtgctccat ccttttctgc ctgagtcctc cttatctgag agtggtcatg aaccactcac 180 235 cacctactct tctggaggct tcagaggagc tacagtgaaa taaaagccgc attgc <210> <211> <212> PRT <213> Conus catus <400> 76 Ser Thr Arg Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser <210> 77 <211> 28 <212> PRT <213> Conus catus <220> <221> PEPTIDE <222> (1)..(28)Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 3 is <223> Pro or Hy <400> 77 Cys Leu Xaa Ala Gly Xaa Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser 20 <210> 78 <211> 227 <212> DNA <213> Conus catus <400> 78 tcgacacgct gccagggtag aggaggacca tgtactaagg ctgtgtttaa ctgctgcagc 60 120 qqttcttqca acaqaqqtag atgtggctga tccagcgcct gatcttcccc cttctgtgct ctatectttt etgeetgagt ceteettact gagagtagte atgaaceact cateacetae 180

tcctctggag gcctcagaga gctacattga aataaaagcc gcattgc	227
<210> 79 <211> 29 <212> PRT <213> Conus catus	
<pre><400> 79 Ser Thr Arg Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe 1</pre>	
Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly 20 25	
<210> 80 <211> 25 <212> PRT <213> Conus catus	
<220> <221> PEPTIDE <222> (1)(25) <223> Xaa at residue 7 is Pro or Hyp	
<pre><400> 80 Cys Gln Gly Arg Gly Gly Xaa Cys Thr Lys Ala Val Phe Asn Cys Cys 1 10 15</pre>	
Ser Gly Ser Cys Asn Arg Gly Arg Cys 20 25	
<210> 81 <211> 236 <212> DNA <213> Conus catus	
<400> 81 ttaactttgc gctgcgcaac ttacggaaaa ccttgtggta ttcaaaacga ctgctgcaat	60
acatgogato cagocagaaa gacatgtaog tagotgatoo ggogtotgat otcoccoott	120
ctgtgctcta tecttttetg cetgagteet eettaeetga gagtggteat gaaccaetea	180
tcacctgctc ctctggaggc ctcgggggag ctacattgaa ataaaagccg cattgc	236
<210> 82 <211> 30 <212> PRT <213> Conus catus	
<400> 82 Leu Thr Leu Arg Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn 1 5 10 15	
Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr 20 25 30	
<210> 83 <211> 26 <212> PRT <213> Conus catus	
<220> <221> PEPTIDE	

```
<2.2.2>
      (1)..(26)
      Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
<223>
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 83
Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
       84
<210>
       229
<211>
<212>
      DNA
<213>
      Conus catus
<400> 84
tcgactcgct gccggggtag aggaggacca tgtactaagg ctatgtttaa ctgctgcagc
                                                                       60
ggttcttgca acagaggtag atgtggctga tccagcgcct gatcttcccc cttctgtgct
                                                                      120
ctatcctttt ctgcctgagt cctccttaac tgagagtagt catgaaccac tcatcaccta
                                                                      180
                                                                      229
ctcctctgga ggcctcagag aagcatcatt gaaataaaag ccgcattgc
       85
<210>
<211>
       29
<212>
       PRT
<213> Conus catus
<400> 85
Ser Thr Arg Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe
Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly
                                 25
             20
<210> 86
<211> 25
<212> PRT
<213> Conus catus
<220>
        PEPTIDE
 <221>
 <222>
       (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp
 <400> 86
 Cys Arg Gly Arg Gly Gly Xaa Cys Thr Lys Ala Met Phe Asn Cys Cys
 Ser Gly Ser Cys Asn Arg Gly Arg Cys
             20
 <210>
        87
 <211>
        374
 <212>
        DNA
 <213>
       Conus circumcisus
 <400> 87
                                                                      60
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg
                                                                       120
```

```
180
aggtoggaca ccaaactoco catgtogact ogotgoaagg gtaaaggago atcatgtogt
aagactatgt ataactgctg cagcggttct tgcagcaacg gtagatgtgg ctgatccagc
                                                                      240
gcctgatctt cccccttctg ctgctctatc cttttctgcc tgagtcctcc ttacctgaga
                                                                      300
gctggtcatg aaccactcat cacctgctcc tctggaggcc cagaggagct acattgaaat
                                                                      360
                                                                      374
aaaagccgca ttgc
<210>
       88
       71
<211>
<212>
       PRT
       Conus circumcisus
<213>
<400> 88
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Thr
                                                         15
                                     1.0
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Gly
Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys Ser Gly Ser
Cys Ser Asn Gly Arg Cys Gly
65
<210>
       89
       25
<211>
<212>
       PRT
       Conus circumcisus
<213>
<220>
<221>
      PEPTIDE
<222>
       (1)..(25)
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 89
Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys
Ser Gly Ser Cys Ser Asn Gly Arg Cys
<210>
       90
<211>
       379
<212>
       DNA
<213>
       Conus circumcisus
<400>
       90
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                        60
                                                                       120
acquectqtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
aggtcggcca ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgccgc
                                                                       180
                                                                       240
tctactacga gaacctgctg cggttattgc tcttatttca gcaaaaaatg tattgacttt
```

cccaqcaact gatcttcccc ctactgtgct ctatcctttt ctgcctgagt cctccttacc

tgagagtggt catgaaccac tcatcaccct actcctctgg aggcccagag gagctacatt	360
gaaataaaag ccgcattgc	379
<210> 91 <211> 77 <212> PRT <213> Conus circumcisus	
<400> 91	
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr 1 5 10 15	
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg 20 25 30	
Ala Leu Arg Ser Ala Thr Lys Val Ser Lys Ser Thr Ser Cys Met Glu 35 40 45	
Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys 50 60	
Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe Pro Ser Asn 65 70 75	
<210> 92 <211> 35 <212> PRT <213> Conus circumcisus	
<pre><220> <221> PEPTIDE <222> (1)(35) <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue s Pro or Hyp; Xaa at residue 10, 21 and 24 is Tyr, 125I-Tyr, -iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty</pre>	33 i mono
<pre><400> 92 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg 1</pre>	
Thr Cys Cys Gly Xaa Cys Ser Xaa Phe Ser Lys Lys Cys Ile Asp Phe 20 25 30	
Xaa Ser Asn 35	
<210> 93 <211> 379 <212> DNA <213> Conus circumcisus	
<400> 93 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg	60
acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg	120
aggtoggaca ccaaactoco catgtogact ogotgoaaga gtaaaggago aaaatgttoa	180
aggettatgt atgaetgetg cageggttet tgeageaggt acteaggtag atgtggetga	240
tocagogoot gatottocoo ettotgotgo totatoottt totgootgag tootoottac	
	300

gaaataaaag ccgcattgc	379
<210> 94 <211> 73 <212> PRT <213> Conus circumcisus	
<pre><400> 94 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr 1</pre>	
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg 20 25 30	
Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Ser 35 40 45	
Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser 50 55	
Cys Ser Arg Tyr Ser Gly Arg Cys Gly 65 70	
<210> 95 <211> 27 <212> PRT <213> Conus circumcisus	
<220> <221> PEPTIDE <222> (1)(27) <223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, diTyr, O-sulpho-Tyr or O-phospho-Ty	iodo
<400> 95 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys 1 5 10	
Ser Gly Ser Cys Ser Arg Xaa Ser Gly Arg Cys 20 25	
<210> 96 <211> 379 <212> DNA <213> Conus circumcisus	
<400> 96 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg	60
acgacetgte aacteateae agetgatgae teeagaggta egeagaagea tegtteeetg	120
acgtcggcca ccaaagtctc caagtcgact ggctgcatga aagccggatc ttattgccgc	180
tctactacga gaacttgctg cggttattgc gcttatttcg gcaaaaaatg tattgactat	240
cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctaagt cctccttacc	300
tgagagtggt catgaaccac tcatcaccct actcctctgg aggcccagag gagctacatt	360
gaaataaaag ccgcattgc	379
<210> 97 <211> 77 <212> PRT <213> Conus circumcisus	

```
<400> 97
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ser Leu Thr Ser Ala Thr Lys Val Ser Lys Ser Thr Gly Cys Met Lys
Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
                    70
<210>
       98
       35
<211>
<212>
       PRT
<213> Conus circumcisus
<220>
      PEPTIDE
<221>
<222>
      (1)..(35)
      Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
        is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
       phospho-Ty
<400> 98
Ser Thr Gly Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
Xaa Ser Asn
<210>
       99
<211>
       362
<212>
       DNA
<213>
       Conus consors
<400> 99
                                                                       60
atqaaactqa cqtqtqqt qatcqtcqcc gtgctgctcc tgacggcctg tcaactcctc
acagctgatg actccagagg tacgcagaag catcgtgccc tgaagtctta caccaaactc
                                                                      120
                                                                      180
tecatqttaa etttqeqetq eqeatettae ggaaaacett gtggtattga caacgactge
tgcaatacat gcgatccagc cagaaagaca tgtacgtagc tgatccggcg tctgatcttc
                                                                       240
coccttctqt gctctatcct tttctgcctg agtcctcctt acctgagagt ggtcatgaac
                                                                       300
                                                                       360
cactcatcac ctaqctcctc tqgaggcttc agaggagcta caatgaaata aaagcgcatt
                                                                       362
gc
<210>
       100
<211>
       72
<212>
       PRT
<213>
      Conus consors
<400> 100
```

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Lys Ser Tyr Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr <210> 101 <211> 26 <212> PRT <213> Conus consors <220> PEPTIDE <221> <222> (1)..(26)Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty <400> 101 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr <210> 102 <211> 237 <212> DNA <213> Conus consors <400> 102 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60 acagetgatg actecagagg tacgeagaag categtgeee tgaggtegga caceaaacte 120 tccatgtcga ctcgctgcaa gggtacagga aaaccatgca gtaggattgc gtataactgc 180 237 tgcaccggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgatc tcccccc 103 <210> <211> 71 PRT <212> <213> Conus consors <400> 103 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser

55

```
Cys Arg Ser Gly Lys Cys Gly
<210> 104
<211>
<212> PRT
<213> Conus consors
<220>
<221>
      PEPTIDE
<222>
       (1)..(25)
       Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
<223>
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 104
Cys Lys Gly Arg Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
                                                        15
                                    10
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210>
       105
<211>
       320
<212> DNA
<213> Conus consors
<400> 105
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc
                                                                       60
acagetgatg actecaaagg tacgeagaag categtteec tgaggtegae caccaaagte
                                                                      120
tccaaggcga ctgactgcat tgaagccgga aattattgcg gacctactgt tatgaaaatc
                                                                      180
                                                                      240
tgctgcggct tttgcagtcc atacagcaaa atatgtatga actatcccca aaattgatct
                                                                      300
tececettet gtgetetate ettttetgee tgagteetee ttacetgaga gtggteatga
                                                                      320
accactcatc acctcgtccc
<210> 106
<211>
       78
<212>
       PRT
<213>
       Conus consors
<400> 106
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Lys Gly Thr Gln Lys His Arg
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
 Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
 Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Gln Asn
 <210>
        107
 <211>
        36
 <212> PRT
 <213> Conus consors
```

```
<220>
       PEPTIDE
<221>
<222>
      (1)..(36)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
       25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125
       I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 107
Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
Xaa Xaa Gln Asn
<210>
       108
<211>
       321
<212>
       DNA
<213>
       Conus consors
<400> 108
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc
                                                                       60
                                                                      120
acagetgatg actecagagg tacgeagaag categtgeec tgaggtegga caecaaacte
tccatgtcga ctcgctgcaa aggtaaagga gcatcatgta caaggcttat gtatgactgc
                                                                      180
                                                                      240
tgccacggtt cttgcagcag cagcaagggt agatgtggct gatccggcgc ctgatcttcc
cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagaggt ggtcatgaac
                                                                      300
                                                                      321
cactcatcac ctgctcccct g
<210>
       109
       73
<211>
<212>
       PRT
<213> Conus consors
<400> 109
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys His Gly Ser
 Cys Ser Ser Lys Gly Arg Cys Gly
 <210>
       110
 <211>
        27
 <212>
       PRT
 <213>
       Conus consors
 <220>
 <221> PEPTIDE
```

```
<222>
      (1)..(27)
      Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
       -sulpho-Tyr or O-phospho-Ty
<400> 110
Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Xaa Asp Cys Cys
His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys
       111
<210>
<211>
       292
<212>
       DNA
<213>
       Conus consors
<400> 111
ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa
                                                                       60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc
                                                                      120
aaactctcca tgtcaactcg ctgcaagggt aaaggagcat catgtcatag gacttcgtat
                                                                      180
gactgctgca ccggttcttg caacagaggt aaatgtggct gatccggcgc ctgatcttcc
                                                                      240
                                                                       292
cccttctqtq ctctatcctt ttctgcctga gtcatccata cctgtgctcg ag
<210>
       112
<211>
       71
<212>
       PRT
<213>
       Conus consors
<400> 112
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Thr Ala
                                     10
                                                         15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
Cys Asn Arg Gly Lys Cys Gly
<210>
       113
<211>
       25
<212>
       PRT
<213>
       Conus consors
<220>
<221>
       PEPTIDE
       (1)..(25)
<222>
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
       -sulpho-Tyr or O-phospho-Ty
<400> 113
Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
Thr Gly Ser Cys Asn Arg Gly Lys Cys
```

```
<210> 114
<211> 299
<212> DNA
<213> Conus consors
<400> 114
ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa
                                                                       60
                                                                      120
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgaa gtcggacacc
                                                                      180
aaactctcca tgttaacttt gcgctgcgca tcttacggaa aaccttgtgg tatttacaac
gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg
                                                                      240
atcttccccc ttctgtgctc tatccttttc tgcctgagtc atccatacct gtgctcgag
                                                                      299
<210> 115
<211> 72
<212> PRT
<213> Conus consors
<400> 115
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
Asp Pro Ala Arg Lys Thr Cys Thr
                    70
65
<210> 116
<211> 26
<212>
       PRT
<213> Conus consors
<220>
<221> PEPTIDE
<222>
       (1)..(26)
       Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
<400> 116
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
             20
<210>
       117
<211>
       434
       DNA
<212>
<213>
       Conus consors
<220>
<221> misc feature
```

<400> 120

```
<222>
      (1)...(434)
      n may be any nucleotide
<223>
<400> 117
ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa
                                                                   60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc
                                                                  120
                                                                  180
aaactctcca tgtcgactcg ctgcaagggt acaggaaaac catgcagtag ggttgcgtat
aactgctgca ccggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc
                                                                  240
cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagagtg gtcatgaacc
                                                                  300
                                                                   360
actcatcacc tgctcctctg gaggcttcag aggagctaca ttgaaataaa agccgcattg
420
                                                                   434
aaaaaaaaa aaaa
<210> 118
<211> 71
<212> PRT
<213> Conus consors
<400> 118
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
                                   10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser
Cys Arg Ser Gly Lys Cys Gly
<210>
       119
<211>
       25
<212>
       PRT
<213> Conus consors
<220>
      PEPTIDE
<221>
<222>
       (1)..(25)
       Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 119
Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys 20 25
<210>
       120
<211>
       393
<212>
      DNA
<213>
      Conus consors
```

```
ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa
                                                                       60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc
                                                                      120
aaagteteca agtegaetag etgeatgaaa geegggtett attgeegete taetaegaga
                                                                      180
acctgctgcg gttattgcgc ttatttcggc aaattttgta ttgactttcc cagcaactga
                                                                      240
                                                                      300
tettececet actgtgetet atectttet geetetgeet gagteeteet taeetgagag
tggtcatgaa ccactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata
                                                                      360
                                                                      393
aaagccgcat tgcaaaaaaa aaaaaaaaaa aaa
<210>
      121
<211>
       77
<212>
      PRT
      Conus consors
<213>
<400> 121
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
                             40
Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn
<210>
       122
<211>
       35
       PRT
<212>
<213> Conus consors
<220>
       PEPTIDE
<221>
        (1)..(35)
<222>
       Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21 and 24 is
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
        pho-Ty
 <400> 122
 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe
 Xaa Ser Asn
         35
 <210>
        123
 <211>
        361
 <212>
        DNA
        Conus dalli
 <213>
 <400> 123
```

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttcctg

```
120
acggcctgtc aactcatcac agctgatgac tccagaagta cgcagaagca tcgtgctctg
aggtcgacca tcaaacactc catgttgact aggagctgca cgcctcccgg aggaccttgt
                                                                      180
                                                                      240
ggttattata atgactgctg cagtcatcaa tgcaatataa gcagaaataa atgcgagtag
ctgatccggc atctgatctt ccccttctgt gctcgtccta acctgagagt ggtcatgaac
                                                                      300
catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg
                                                                      360
                                                                      361
C
<210>
      124
      73
<211>
<212>
      PRT
<213>
       Conus dalli
<400> 124
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr
Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
Cys Asn Ile Ser Arg Asn Lys Cys Glu
65
<210> 125
<211>
       28
<212>
       PRT
<213>
       Conus dalli
<220>
<221>
       PEPTIDE
<222>
       (1)..(28)
       Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4,
<223>
        5 and 8 is Pro or Hyp; Xaa at residue 11 and 12 is Tyr, 1251-Tyr,
        mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 125
Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys
                                     10
Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa
<210>
        126
        350
<211>
<212>
       DNA
<213>
       Conus distans
<400> 126
accaaaacca tcatcaaaat gaaactgacg tgcgtgttga tcatcgccgt gctgttcctg
                                                                        60
 acggcctgtc aactcactag aggaaagctg gagcgtcctg ttctgaggtc gagcgaccaa
                                                                       120
                                                                       180
 acctccqqqt caacqaaqag atgcgaagat cctggtgaac cttgcggaag tgatcattcc
```

tgctgcggcg gtagttgcaa ccacaacgtc tgcgcctgaa gctggtctgg catctgacca

tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata 350									
tototoaata cottotocoo tggaggotto agaagaacta gattgaaata 35									
<210> 127 <211> 66 <212> PRT <213> Conus distans									
<400> 127									
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala 1 5 10 15									
Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser 20 25 30									
Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro 35 40 45									
Cys Gly Ser Asp His Ser Cys Cys Gly Gly Ser Cys Asn His Asn Val 50 55 60									
Cys Ala 65									
<210> 128									
<211> 25 <212> PRT <213> Conus distans									
<220>									
<221> PEPTIDE <222> (1)(25)									
<pre><223> Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu; Xaa at residu e 4 and 7 is Pro or Hy</pre>									
<400> 128 Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly									
1 5 10 15									
. 10									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129 <211> 309									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129 <211> 309 <212> DNA									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129 <211> 309 <212> DNA <213> Conus ermineus <400> 129									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129 <211> 309 <212> DNA <213> Conus ermineus <400> 129 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129 <211> 309 <212> DNA <213> Conus ermineus <400> 129 atgaaactga cgtgtgtgt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60 acagctgacg actccagacg tacgcagaag catcgtgccc tgaggtcgac caccaaacgc 120									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129 <211> 309 <212> DNA <213> Conus ermineus <400> 129 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60 acagctgacg actccagacg tacgcagaag catcgtgccc tgaggtcgac caccaaacgc 120 gccacgtcga atcgccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac 180									
1 5 10 15 Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <210> 129 <211> 309 <212> DNA <213> Conus ermineus <400> 129 atgaaactga cgtgtgtgt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60 acagctgacg actccagacg tacgcagaag catcgtgccc tgaggtcgac caccaaacgc 120 gccacgtcga atcgccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac 180 tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttcccctt ctgtgctgta 240									
Gly Ser Cys Asn His Asn Val Cys Ala 20 25 <pre> <210> 129 <211> 309 <212> DNA <213> Conus ermineus <400> 129 atgaaactga cgtgtgtgt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcate 60 acagctgacg actccagacg tacgcagaag catcgtgccc tgaggtcgac caccaaacgc 120 gccacgtcga atcgccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac 180 tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttccccctt ctgtgctgta 240 tccttttctg cctgagtcct ccttacctga gagtggtcag taaccactca tcaccatctc 300</pre>									

```
<213> Conus ermineus
<400> 130
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
                                    10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Asn Lys
Thr Cys Thr Arg Ser Lys Cys Pro
<210> 131
<211> 27
<211> 27
<212> PRT
<213> Conus ermineus
<220>
<221> PEPTIDE
<222>
       (1)..(27)
      Xaa at residue 1, 4, 11 and 27 is Pro or Hyp
<400> 131
Xaa Xaa Lys Xaa Lys Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Xaa
<210>
       132
<211>
       308
<212> DNA
<213> Conus ermineus
<400> 132
aactcatcac agctgatgac tccagaggta cgcagaacga tcgtgccctg aggtcgacca
                                                                        60
ccaaactctc catgctgact cgggcctgct ggtcttccgg aacaccttgt ggtactgata
                                                                      120
gtttatgctg cggtggatgc aatgtatcca aaagtaaatg taactagctg attcggcgtc
                                                                      180
                                                                       240
tgaacttccc ccttctgtgc tctatccttt tctgcccgag tcctccatac ctgagaatgg
tcatgaacca ctcatcacct actcctctgg agacctcaga agagctacac tgaaataaaa
                                                                       300
                                                                       308
gcgcttgc
<210> 133
<211> 54
<212> PRT
<213> Conus ermineus
<400> 133
Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Asn Asp Arg Ala Leu
Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Ala Cys Trp Ser Ser
```

```
Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val
Ser Lys Ser Lys Cys Asn
    50
<210> 134
<211> 27
<212> PRT
<213> Conus ermineus
<220>
      PEPTIDE
<221>
<222>
      (1)..(27)
      Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
<223>
<400> 134
Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
<210>
       135
<211>
       385
<212>
       DNA
<213> Conus geographus
<400> 135
ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa
                                                                       60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctggg gtcgaccacc
                                                                      120
gaacteteet tgtegaeteg etgeaagtea eeeggatett eatgtteaee gaetagttat
                                                                      180
aattgctgca ggtcttgcaa tccatacgcc aaaagatgtt acggctaatc cagcgcctga
                                                                      240
tettececet tetgtgetet atceetteet gtetgagtee teettacetg agagtggtea
                                                                      300
                                                                      360
tgaaccactc ctcacctact tctctggagg cttcggagga gctacattga aataaaagcc
                                                                      385
qcattgtaaa aaaaaaaaaa aaaaa
       136
<210>
<211>
       73
<212> PRT
<213> Conus geographus
<400> 136
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
 Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
Asn Pro Tyr Ala Lys Arg Cys Tyr Gly 65
```

<210><211><211><212><213>	137 27 PRT Conus geographus	
<220> <221> <222> <223>	PEPTIDE (1)(27) Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Ty or O-phospho-Ty	r
<400> Cys Ly 1	137 s Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys 5 10 15	
Arg Se	r Cys Asn Xaa Xaa Ala Lys Arg Cys Xaa 20 25 `	
<210> <211> <212> <213>	DNA	
<400>	138 atga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 6	0
	acag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcgtccacc 12	0
aaacto	cacct tgtcgactcg ctgcaaatca cccggaactc catgttcaag gggtatgcgt 18	0
gattgo	etgca egeettgett gttatacage aacaaatgta ggegetacta acceagegee 24	0
tgatct	toco cottotgtgo totattoott totgootgag tootoottac otgaaagtgg 30	0
tcatga	aacca ctcatcacct acttctctgg aggcttcaga agagctacat tgaaataaaa 36	0
gccgca	attgc aatgacaaaa aaaaaaaaa aaaaaa 39	6
<210> <211> <212> <213>	PRT	
<400> Met Ly 1	139 ys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala 5 10 15	
Cys G	ln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg 20 25 30	
Ala L	eu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser 35 40 45	
Pro G 5	ly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys 0 55 60	
Leu L 65	eu Tyr Ser Asn Lys Cys Arg Arg Tyr 70	
<210><211><212><213>	29 PRT	

```
<220>
      PEPTIDE
<221>
<222>
      (1)..(29)
      Xaa at residue 4, 7 and 18 is Pro or Hyp; Xaa at residue 22 and 2
<223>
       9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
       -phospho-Ty
<400> 140
Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
Thr Xaa Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
<210> 141
<211> 407
<212>
      DNA
      Conus geographus
<213>
<400> 141
ggaattccgt ttctgcgctg cttcctttgg catcaccaaa accatcatca aaatgaaact
                                                                       60
gacgtgtgtg gtgatcgtcg ccgtgctgct cctgacggcc tgtcaactca tcacagctga
                                                                      120
tgactccaga ggtacgcaga agcatcgtgc cctggggtcg accaccgaac tctccttgtc
                                                                      180
gactcgctgc aagtcacccg gatcttcatg ttcaccgact agttataatt gctgcaggtc
                                                                      240
ttgcaatcca tacaccaaaa gatgttacgg ctaatccagc gcctgatctt ccctgctctg
                                                                      300
agtectectt acctgagagt ggteatgaac cacteateac etaettetet aggeggtteg
                                                                      360
                                                                      407
gaggagctac attgaaataa aagccgcatt gcaaaaaaaa aaaaaaa
<210>
       142
       73
<211>
<212>
       PRT
<213> Conus geographus
<400> 142
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
                                     10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
                                 25
Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
 Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
 Asn Pro Tyr Thr Lys Arg Cys Tyr Gly
                     70
 <210> 143
 <211> 27
 <212> PRT
 <213> Conus geographus
 <220>
 <221>
        PEPTIDE
 <222>
        (1)..(27)
        Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
        and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
```

or O-phospho-Ty <400> 143 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa 20 <210> 144 <211> 28 <212> PRT <213> Conus geographus <220> <221> PEPTIDE <222> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22 <223> and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty <400> 144 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys 5 10 Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly 25 <210> 145 <211> 26 <212> PRT <213> Conus geographus <220> <221> PEPTIDE <222> (1)..(26)Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and <223> 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty <400> 145 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys 10 15 Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys 20 <210> 146 <211> 314 <212> DNA <213> Conus geographus <400> 146 catcacaget gatgaeteca gaggtaegea gaageategt geeetgaggt egteeaceaa 60 120 acteacettg tegacteget geaaateace eggaacteea tgtteaaggg gtatgegtga ttgctgcacg tcttgcttgt tatacagcaa caaatgtagg cgctactaac ccagcgcctg 180

atottccccc ttctgtgctc tattcctttc tgcctgagtc ctccttacct gaaagtggtc

atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaagc

cgcattgcaa tgac

240

300

```
<210>
      147
<211>
      55
      PRT
<212>
<213>
      Conus geographus
<400> 147
Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg
                                    10
Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr
            20
Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr
                            40
Ser Asn Lys Cys Arg Arg Tyr
<210>
      148
<211>
      29
<212> PRT
<213> Conus geographus
<220>
<221>
      PEPTIDE
<222>
       (1)..(29)
<223>
       Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
<400> 148
Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
                                    10
                                                         15
Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
<210>
      149
<211>
       29
<212>
      PRT
<213>
      Conus geographus
<220>
      PEPTIDE
<221>
<222>
      (1)..(29)
      Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
<223>
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
<400> 149
Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa
<210>
      150
<211>
       380
<212>
      DNA
<213>
      Conus laterculatus
<400> 150
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                       60
acggcctgtc aactcatcac cgctgatgac tccagaggta cgcagaagca tcgtgccctg
                                                                      120
```

aggtcgacca														180
cgtgcgaata	a gtaaa	tgct	g ca	gtgg	atgc	gat	cgga	aca	gaaa	taaa	tg t	tact	agctg	240
attcggcgtd	c tgaac	ttcc	t cc	ttct	gtgc	tct	atco	ttt	tctg	cccg	rag t	cctc	catac	300
ctgagagtg	g tcato	gaacc	a ct	caac	tcct	. act	cctc	tgg	aggo	ctca	ıga a	agago	ctacat	360
tgaaataaa	a gccgc	cattg	(C											380
<210> 153 <211> 72 <212> PR <213> Con		ercu	ılatu	ıs										
<400> 15 Met Lys Lo	1 eu Thr	Cys 5	Val	Val	Ile	Val	Ala 10	Val	Leu	Leu	Leu	Thr 15	Ala	
Cys Gln L	eu Ile 20	Thr	Ala	Asp	Asp	Ser 25	Arg	Gly	Thr	Gln	Lys 30	His	Arg	
Ala Leu A		Thr	Thr	Asn	Leu 40	Ser	Met	Leu	Thr	Arg 45	Lys	Cys	Trp	
Pro Ser G 50	ly Ser	Tyr	Cys	Arg 55	Ala	Asn	Ser	Lys	Cys 60	Cys	Ser	Gly	Cys	
Asp Arg A 65	sn Arg	Asn	Lys 70	Cys	Tyr									
<210> 15 <211> 27 <212> PR <213> Co		terc	ulatı	ıs										
<pre><220> <221> PEPTIDE <222> (1)(27) <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo</pre>														
<400> 15 Lys Cys X 1	52 Kaa Xaa	Ser 5	Gly	Ser	Xaa	Cys	Arg 10	Ala	Asn	Ser	Lys	Cys 15	Cys	
Ser Gly (Cys Asp 20	Arg	Asn	Arg	Asn	Lys 25	Cys	Xaa						
		iterc	ulat	us										
<400> 15	53 ca tcat	caaa	at g	aaac	tgac	g to	ıtgtç	gtga	ı tcg	rtcgc	cgt	gctg	sctcctg	60
acggcctgt	tc aact	cato	ac a	.gctg	atga	c to	caga	iggta	a aga	agaa	ıgca	tcgt	gccctg	120
aggtcgaco	ca ccaa	acto	tc c	atat	cgac	t c <u>c</u>	gctgc	ccttc	cto	ccgc	gato	atat	tgtaag	180
gcgacaac	gg aagt	ctgc	tg c	tctt	cttg	sc ct	tcaa	attc	gcto	cagat	atg	ttc	ggttga	240

7)	
tettecetet tetgtgetet ateetttet geetgagtee tecatacetg agaatggtea 300	
tgaaccactc aacatctact cctctggagg cctcagaaga gctatattga aataaaagcc 360	
gcattgc 367	
<210> 154 <211> 73 <212> PRT <213> Conus laterculatus	
<400> 154 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala 1 5 10 15	
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg 20 25 30	
Ala Leu Arg Ser Thr Thr Lys Leu Ser Ile Ser Thr Arg Cys Leu Pro 35 40 45	
Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys Ser Ser Cys 50 55 60	
Leu Gln Phe Ala Gln Ile Cys Ser Gly 65 70	
<210> 155 <211> 27 <212> PRT <213> Conus laterculatus	
<pre><220> <221> PEPTIDE <222> (1)(27) <223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 a nd 4 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo- Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty</pre>	
<400> 155 Cys Leu Xaa Xaa Gly Ser Xaa Cys Lys Ala Thr Thr Xaa Val Cys Cys 1 5 10 . 15	
Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser 20 25	
<210> 156 <211> 373 <212> DNA <213> Conus laterculatus	
<400> 156 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60)
acggeetgte aacteateae agetgatgae teeagaggta egeagaagea tegtgeeetg 120)
aggtcgacca ccaatctctc catgtcgact cgctgcaagt ctcccggatc atcatgtage 180)
gtgtctatgc gtaactgctg cacttcttgc aattcacgca ccaagaaatg tacgcgacgt 240)
ggctgaactt cccccttctg tgctctatcc ttttctgccc gagtcctcca tacctgagag 300)
tggtcatgaa ccactcaaca tctactcctc tggaggcctc agaagagcta tattgaaata 360)
aaagccgcat tgc 373	;

```
<210> 157
<211> 75
<212> PRT
<213> Conus laterculatus
<400> 157
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys Thr Ser Cys
Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg Gly
<210> 158
<211> 29
<212> PRT
<213> Conus laterculatus
<220>
       PEPTIDE
<221>
<222>
      (1)..(29)
     Xaa at residue 3 is Pro or Hyp
<223>
<400> 158
Cys Lys Ser Xaa Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
                                    10
Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
<210> 159
<211>
       330
<212>
       DNA
<213> Conus laterculatus
<400> 159
accaaaacca tcatcaaaat qaaactqacq tgtgtggtga tcgtcgccgt gctgctcctg
                                                                      60
                                                                     120
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
aggtcgacaa ccaaactctc catgctgact cggacctgct ggccttccgg aacagcttgt
                                                                     180
ggtattgata gtaactgctg cagtggatgc aatgtatcca gaagtaaatg taactagctg
                                                                     240
atteggegte taaactteet eettetgeet gagteeteea taeetgagag tggteatgaa
                                                                     300
                                                                     330
ccacatcatc acctcatctc tggaggcctc
<210>
       160
<211>
       72
<212> PRT
<213> Conus laterculatus
<400> 160
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
                5
                                    10
```

```
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
                                25
            20
Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Thr Cys Trp
Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys Ser Gly Cys
Asn Val Ser Arg Ser Lys Cys Asn
<210> 161
<211> 27
<212> PRT
<213> Conus laterculatus
<220>
<221>
      PEPTIDE
<222>
      (1)..(27)
<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
<400> 161
Thr Cys Xaa Xaa Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
                                    10
Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
<210>
       162
       363
<211>
<212>
       DNA
       Conus laterculatus
<213>
<400> 162
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                       60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
                                                                      120
aggtcgacca ccaatctctc catgctgact cggaagtgct ggccttccgg aagctattgt
                                                                      180
cgtgcgaata gtaaatgctg cagtggatgc gatcggaaca gaagtaaatg taactagctg
                                                                      240
atteggegte taaactteet cettetgeet gagteeteea taeetgagag tggteatgaa
                                                                      300
                                                                      360
ccactcatca cctactcctc tggaggcctc aaaggagcta cattgaaata aaagccgcat
                                                                      363
tqc
<210> 163
<211>
       72
<212>
      PRT
<213> Conus laterculatus
<400> 163
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
```

40

```
Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys
Asp Arg Asn Arg Ser Lys Cys Asn
<210>
      164
<211>
      27
<212> PRT
<213> Conus laterculatus
<220>
<221>
      PEPTIDE
<222>
      (1)..(27)
      Xaa at residue4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
      Trp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Ty
<400> 164
Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys
Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
<210>
      165
<211>
      391
<212> DNA
<213> Conus leopardus
<220>
<221>
      misc_feature
<222>
      (1)..(391)
<223> n may be any nucleotide
<400> 165
atgaaactga cgtgtgtggt gatcgtagct gtgctgttcc tgacggcctg tcaactcact
                                                                      60
acagetgaca tetecagagg taegeggaag egtegtgete tgaggtegae caecaaacte
                                                                     120
tocaggtogo totttgagtg ogogoottoo ggtggacgtt gtggtttttt aaagtootgo
                                                                     180
tgcgaaggat attgcgatgg ggaaagcact tcatgtgtga gtggcccata cagcatctqa
                                                                     240
tettecegee tteagtgete tateetttte tgeetgagte etceatacet etgageggte
                                                                     300
atgaaccact caacacctac tcctctggag gcttcaggga actatattaa aataaagccg
                                                                     360
cattgcaacg aaanaaaaaa aaaaaaaaa a
                                                                     391
<210>
      166
      79
<211>
<212>
      PRT
<213> Conus leopardus
<400> 166
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys Arg Arg
Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala
        35
                            40
```

```
Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys Ser Cys Cys Glu Gly Tyr
                        55
Cys Asp Gly Glu Ser Thr Ser Cys Val Ser Gly Pro Tyr Ser Ile
<210>
      167
<211>
      37
<212> PRT
<213> Conus leopardus
<220>
<221>
       PEPTIDE
<222>
       (1)..(37)
       Xaa at residue 4, 20 and 26 is Glu or gamma-carboxy Glu; Xaa at r
<223>
       esidue 7 and 34 is Pro or Hyp; Xaa at residue 22 and 35 is Tyr,
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
<400> 167
Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys
Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser
Gly Xaa Xaa Ser Ile
        35
<210>
       168
<211>
       365
<212>
       DNA
<213>
       Conus leopardus
<400> 168
atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact
                                                                       60
acagctgaca tctccagagg tacgtggaag catcgtggtg tggggtcgac caccggactc
                                                                      120
tccccgtggc ccttggactg cacggctccc agtcaacctt gtggttattt tcctaggtgc
                                                                      180
tgtggacatt gcgatgtacg cagggtatgt acgagtggct gatccggcgt ctgatctttc
                                                                       240
                                                                       300
egecttetqt getgtateet tttetgeetg agteeteeat accegtgagt ggteatgaae
cactcaacac ctactcctct ggaggcttca gaggaactat attaaaataa agccgcattg
                                                                       360
                                                                       365
caatg
<210>
       169
       73
<211>
<212>
       PRT
       Conus leopardus
<213>
<400> 169
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg
Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr
```

```
Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys
Asp Val Arg Arg Val Cys Thr Ser Gly
65
<210> 170
<211>
       30
<212>
      PRT
<213> Conus leopardus
<220>
<221>
       PEPTIDE
<222>
       (1)..(30)
       Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa at residue 1 is
<223>
        Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-
       Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 170
Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa
Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
<210>
       171
<211>
       381
<212>
       DNA
<213>
      Conus leopardus
<400> 171
atgaaactga cgtgtgtggt gatcgtcgct gtgctgttcc tgacggcctg tcaactcact
                                                                       60
acagctgaca tctccagagg tacgcggaag catcgtgctc tgaggtcgac caccaaactc
                                                                      120
                                                                      180
tccaggtcgc cctctaggtg catgtctccc ggtggaattt gtggtgattt tggtgactgc
tgcgaaattt gcaatgtgta cggtatatgt gtgagtgact tacccggcat ctgatctttc
                                                                      240
cyccttctgt gctctatcct tttctgcctg agtcctccat acccctgagt ggtcatggac
                                                                      300
cactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattg
                                                                      360
                                                                      381
caaaaaaaaa aaaaaaaaa a
<210> 172
<211> 77
<212> PRT
<213> Conus leopardus
<400> 172
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg
Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met
Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys
Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
                     70
```

```
<210> 173
<211>
      31
<212>
      PRT
<213>
      Conus leopardus
<220>
<221>
      PEPTIDE
<222>
      (1)..(31)
<223>
      Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa at residue 4 a
       nd 29 is Pro or Hyp; Xaa at residue 21 is Tyr, 125I-Tyr, mono-iod
       o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 173
Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa
Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile
<210>
      174
<211> 404
<212> DNA
<213> Conus leopardus
<400> 174
atgaaactga cgtgtgtqqt qatcgtcgct gtgctgttcc tgacggcctg tcaactcact
                                                                      60
acagetgatg attecagagg tacaeggaag categtgete tgaggteaae caccaaacte
                                                                     120
tccagqtggc ccaggtactg cgcgcctccc ggtggagctt gtgggttttt tgatcactgc
                                                                     180
                                                                     240
tgcggatatt gcgaaacgtt ttacaatacg tgtagatgag ttggctgatc cggcgcttga
tettteegee ttetgttget etatettttt etgeetgagt ceteceatae eeegttgagt
                                                                     300
qqtccatqaa ccactccaac acctactccc tccttggaag cttccaaagg aaacgacatt
                                                                     360
                                                                     404
taaaataaat tccccattgc aattggaaaa aaaaaaaaa aaaa
<210>
      175
<211>
      72
<212> PRT
<213> Conus leopardus
<400> 175
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
                                    10
Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg
Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala
                            40
Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys
Glu Thr Phe Tyr Asn Thr Cys Arg
                    70
<210> 176
<211> 27
<212> PRT
<213> Conus leopardus
```

<400> 179

```
<220>
<221>
      PEPTIDE
<222>
      (1)..(27)
      Xaa at residue 20 is Glu or gamma-carboxy Glu; Xaa at residue 4 a
       nd 5 is Pro or Hyp; Xaa at residue 1, 18 and 23 is Tyr, 125I-Tyr,
       mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 176
Xaa Cys Ala Xaa Xaa Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg
            2.0
<210> 177
<211>
      292
<212> DNA
<213> Conus lynceus
<400> 177
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc
                                                                       60
                                                                      120
acagetgatg actecagacg tacacagaag categtgece tgaggtegae caceaatete
tccatgtcga ctcgctgcaa gtctcccgga tcaccatgta gtgtgacatc gtataactgc
                                                                      180
tgcacttttt gctcttcata cactaagaaa tgtcgggcct ctttatgaac cactcatcac
                                                                      240
ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg
                                                                      292
<210>
       178
<211>
       75
       PRT
<212>
<213>
      Conus lynceus
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys
                        55
    50
Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
<210>
       179
<211>
       30
<212>
       PRT
<213> Conus lynceus
<220>
<221>
       PEPTIDE
<222>
       (1)..(30)
       Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22 is
<223>
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
```

```
Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Val Thr Ser Xaa Asn Cys Cys
                                    10
Thr Phe Cys Ser Ser Xaa Thr Lys Lys Cys Arg Ala Ser Leu
                                25
<210> 180
<211> 355
<212>
      DNA
<213> Conus lynceus
<400> 180
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc
                                                                      60
acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgac caccaaacta
                                                                      120
tocatgtata ctcgctgcgc aggtccagga gcaatttgtc ctaatagggt atgctgcggt
                                                                      180
tattgcagta aaagaacaca totatgtcat togcgaactg gotgatotto cocottotgt
                                                                      240
gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa ccactcatca
                                                                      300
cctactcctc ttggagacct cagaggagct acactgaaat aaaagccgca ttggc
                                                                      355
<210>
       181
<211>
       74
<212>
       PRT
<213> Conus lynceus
<400> 181
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
                                    10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
                                                     30
                                25
Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly
Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys
                        55
Arg Thr His Leu Cys His Ser Arg Thr Gly
<210> 182
<211> 28
<212>
       PRT
<213> Conus lynceus
<220>
       PEPTIDE
<221>
<222>
       (1)..(28)
       Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 182
Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
```

```
<210>
      183
<211>
       361
<212>
       DNA
<213> Conus lynceus
<400> 183
atqaaactqa cqtqtqqqt qatcqtcqcc gtqctqctqc taqcqqcctq tcaactacta
                                                                      60
cacqctgatg actccagagg tacgcagaag actgctgccc gaggtcgacc accaaaactc
                                                                     120
tecatgetga etegggeetg etggtettee ggaacacett gtggtaetga tagtttatge
                                                                     180
tgcggtggat gcaatgtatc caaaagtaaa tgtaactagc tgattcggcg tctgaacttc
                                                                     240
ccccttctqt qctctatcct tttctqcccq aqtcctccat acctqagaat gqtcatgaac
                                                                     300
                                                                     360
cactcatcac ctactcctct ggagacctca gaagagctac actgaaataa aagcgcattg
                                                                     361
<210> 184
<211> 72
<212> PRT
<213> Conus lynceus
<400> 184
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Ala Ala
Cys Gln Leu Leu His Ala Asp Asp Ser Arg Gly Thr Gln Lys Thr Ala
Ala Arg Gly Arg Pro Pro Lys Leu Ser Met Leu Thr Arg Ala Cys Trp
Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys
                        55
                                            60
    50
Asn Val Ser Lys Ser Lys Cys Asn
<210> 185
<211>
       27
<212> PRT
<213> Conus lynceus
<220>
      PEPTIDE
<221>
<222>
       (1)..(27)
       Xaa at residue 8 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
<400> 185
Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
<210>
       186
<211>
       364
<212>
       DNA
<213>
       Conus lynceus
<400> 186
```

```
atgaaactga cgtgtgtggt gatcgtcgcc gagctactcc taacggcctg tcaactcatc
                                                                        60
acagetgatq actecagagg tacgeagaag categtgeec tgaggtegac caccaatete
                                                                       120
 tocatgotga ctoggaagtg ctggtotoco ggaacctatt gtogtgogoa tagtaaatgo
                                                                       180
 tgccgtggat gcgatcagaa cagaaataaa tgttactagc tgattcggcg tctgaacttc
                                                                       240
 ctccttctgt gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa
                                                                       300
.ccactcatca cctactcctc tggaggcctc agaggagcct acactgaaat aaaagccgca
                                                                       360
                                                                       364
 ttgg
 <210>
        187
 <211>
        72
 <212>
       PRT
 <213>
       Conus lynceus
 <400> 187
Met Lys Leu Thr Cys Val Val Ile Val Ala Glu Leu Leu Thr Ala
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
                             40
 Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys Arg Gly Cys
Asp Gln Asn Arg Asn Lys Cys Tyr
 65
                     70
 <210>
        188
 <211>
        27
 <212>
       PRT
 <213>
       Conus lynceus
 <220>
 <221>
        PEPTIDE
 <222>
        (1)..(27)
        Xaa at residue 5 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
 <223>
        Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
        iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
 <400> 188
Lys Cys Xaa Ser Xaa Gly Thr Xaa Cys Arg Ala His Ser Lys Cys
                 5
 Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Xaa
 <210>
        189
 <211>
        318
 <212>
        DNA
 <213>
        Conus magus
 <400> 189
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                        60
 acggeetgte aacteateae agetgatgae teeagaggta egeagaagea tegtgeeetg
                                                                       120
 aggtoggaca ccaaactoto catgtogact ogotgcaagg gtacaggaaa accatgcagt
```

```
aggattqcqt ataactgctg caccggttct tgcagatcag gtaaatgtgg ctgatccagt
                                                                     240
gcctgatctt cccccttctg tgctctatcc tttttctgcc tgagtcctcc ttacctgaga
                                                                     300
                                                                     318
gtggtcatga accactca
<210> 190
<211>
      71
<212>
      PRT
<213> Conus magus
<400> 190
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
Cys Arg Ser Gly Lys Cys Gly
<210>
       191
<211>
       25
      PRT
<212>
<213> Conus magus
<220>
       PEPTIDE
<221>
<222>
       (1)..(25)
       Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
<223>
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 191
Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210> 192
       259
<211>
<212> DNA
<213>
      Conus magus
<400> 192
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                      60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
                                                                     120
aagteggaca ccaaactete catgttaact ttgcgctgcg catcttacgg aaaacettgt
                                                                      180
ggtatttaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgtagctg
                                                                      240
atccggcgtc tgatcttcc
                                                                      259
<210>
       193
<211>
       72
<212> PRT
```

```
<213> Conus magus
<400> 193
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
Asp Pro Ala Arg Lys Thr Cys Thr
<210> 194
<211> 26
<212> PRT
<213> Conus magus
<220>
<221> PEPTIDE
<222>
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is
        Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
       spho-Ty
<400> 194
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
<210> 195
<211> 254
<212> DNA
<213> Conus magus
<400> 195
gaattttcag catcaccaaa accatcatca aaatgaaact gacgtgtgtg gtgatcgtcg
                                                                       60
ccgtgctgct cctgacggcc tgtcaactca tcacagctga tgactccaga ggtacgcaga
                                                                      120
                                                                      180
agcatcgtgc cctgaggtcg gacaccaaac tctccatgtc aactcgctgc aagggtaaag
gagcatcatg tcataggact tcgtatgact gctgcaccgg ttcttgcaac agaggtaaat
                                                                      240
                                                                      254
ttggctgatc cgcc
<210> 196
<211> 71
<212> PRT
<213> Conus magus
<400> 196
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
```

```
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
Cys Asn Arg Gly Lys Phe Gly
<210> 197
<211> 25
<212> PRT
<213> Conus magus
<220>
       PEPTIDE
<221>
<222>
       (1)..(25)
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 197
Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
Thr Gly Ser Cys Asn Arg Gly Lys Cys
       198
<210>
<211>
       358
<212>
       DNA
<213>
       Conus miles
<400> 198
qqatccatqa aactqacqtq cqtqqtqatc atcqccatqc tqttcctqac agcctatcaa
                                                                      60
ctcgctacag ctgcgagcta cgccaaaggt aaacagaagc atcgtgctct gaggccagct
                                                                      120
qacaaacacc tcaqqttqac caaqcqttqc aatqatcqcq gtqqaqqttq caqtcaacat
                                                                      180
cctcactgct gcggtggaac ttgcaataag cttattggcg tatgtctgta aagctggtct
                                                                      240
gccgtctgat attccctttc tgtgcttcat cctcttttgc ctgagtcatc catacctgtg
                                                                      300
                                                                      358
aatggttaag agccactcaa tacctattcc tctgggggct tcagaggaac tactttac
<210> 199
<211>
       74
<212>
      PRT
<213> Conus miles
<400> 199
Met Lys Leu Thr Cys Val Val Ile Ile Ala Met Leu Phe Leu Thr Ala
Tyr Gln Leu Ala Thr Ala Ala Ser Tyr Ala Lys Gly Lys Gln Lys His
Arg Ala Leu Arg Pro Ala Asp Lys His Leu Arg Leu Thr Lys Arg Cys
Asn Asp Arg Gly Gly Cys Ser Gln His Pro His Cys Cys Gly Gly
Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
```

```
<210> 200
<211> 27
<212> PRT
<213> Conus arenatus
<220>
<221> PEPTIDE
<222>
       (1)..(27)
      Xaa at residue 12 is Pro or Hyp
<400> 200
Cys Asn Asp Arg Gly Gly Cys Ser Gln His Xaa His Cys Cys Gly
Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
<210>
       201
<211>
       2.92
<212> DNA
<213> Conus monachus
<400> 201
accaaaacca tcatcaaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg
                                                                      60
acggcctqtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
                                                                     120
aggtcggaca ccaaactctc catatcgact cgctgcaagt ctacaggaaa atcatgcagt
                                                                     180
                                                                     240
aggattqcqt ataactqctq caccqgttct tgcagatcag gtaaatgtgg ctgatccagc
                                                                     292
gcctgatctt cccccttctg tgctctatcc ttttctgcct gagtcctcct ta
       202
<210>
<211>
       71
<212> PRT
<213> Conus monachus
<400> 202
Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Lèu Leu Thr Ala
                                    10
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Ser Ile Ser Thr Arg Cys Lys Ser
Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
Cys Arg Ser Gly Lys Cys Gly
<210>
       203
<211>
       2.5
       PRT
<212>
<213>
       Conus monachus
<220>
<221>
       PEPTIDE
<222>
       (1)..(25)
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
<223>
       -sulpho-Tyr or O-phospho-Ty
```

```
<400> 203
Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
            20
<210>
      204
<211>
      258
<212>
      DNA
<213>
      Conus monachus
<400> 204
                                                                      60
accaaaacca tcatcaaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg
                                                                     120
acqqcctqtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
aggtcggaca ccaacctctc catgtcgact cgctgcaagg gtaaaggatc ttcatgtagt
                                                                     180
                                                                     240
aggaccatgt ataactgctg caccggttct tgcaacagag gtaaatgtgg ctgatccagc
                                                                     258
gcctgatctt cccccttc
<210> 205
<211>
      71
      PRT
<212>
<213>
      Conus monachus
<400> 205
Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Gly
Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys Thr Gly Ser
Cys Asn Arg Gly Lys Cys Gly
<210> 206
<211>
      25
<212> PRT
<213> Conus monachus
<220>
      PEPTIDE
<221>
<222>
      (1)..(25)
      Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 206
Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Xaa Asn Cys Cys
                                    10
Thr Gly Ser Cys Asn Arg Gly Lys Cys
<210>
       207
<211> 258
```

```
<212>
      DNA
<213>
     Conus obscurus
<400> 207
                                                                       60
ctctctctct ctctqctqqa caqqtcqcct ccctqcatqa aaggcggatc gtcatqccqc
                                                                      120
qqtactacqq qaqtctqttq cqqtttttgc agtgatttcg gctataaatg tagggactat
ccccaaaact gatetteece ettetgtget etateetttt etgteegagt eeteetgace
                                                                      180
                                                                      240
tgagagtggt catgaaccac tcatcaccta ccctctggg gcttcacagg atctacattg
                                                                      258
aaataaaagc cgcattgc
<210>
      208
<211>
       39
<212>
      PRT
<213>
      Conus obscurus
<400> 208
Leu Leu Asp Arg Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg
1
Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys
                                 25
Cys Arg Asp Tyr Pro Gln Asn
       209
<210>
<211>
       35
<212>
       PRT
<213>
       Conus obscurus
<220>
<221>
       PEPTIDE
<222>
       (1)..(35)
       Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at residue 27 and 3
<223>
       2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
       -phospho-Ty
<400> 209
Ser Xaa Xaa Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
                                     10
Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Xaa Lys Cys Arg Asp Xaa
Xaa Gln Asn
       210
<210>
<211>
       259
<212>
       DNA
<213>
       Conus obscurus
<400> 210
                                                                        60
ctctctctct ctctgctgga caggtcgact cgctgcttgc ctgacggaac gtcttgcctt
tttagtagga tcagatgctg cggtacttgc agttcaatct taaagtcatg tgtgagctga
                                                                       120
tocaqcqqtt gatcttcctc cctctgtgct ccatcctttt ctgcctgagt tctccttacc
                                                                       180
```

tgagagtggt catgaaccac tcatcaccta ctcttctgga ggcttcagag gagctacatt

```
gaaataaaag ccgcattgc
                                                                     259
<210> 211
<211> 32
<212> PRT
<213> Conus obscurus
<400> 211
Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
<210>
      212
<211>
       28
<212> PRT
<213> Conus monachus
<220>
<221>
      PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 3 is Pro or Hyp
<400> 212
Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
<210> 213
<211> 330
<212> DNA
<213> Conus pulicarius
<220>
<221> misc feature
<222> (1)..(330)
<223> n may be any nucleotide
<400> 213
atgaaactga cgtgtgtggt gatcatcgcc gtgctgttcc tgacggcctg tcaactcatt
                                                                     60
acagetgaga ettaeteeag aggtaageag aageaeegtg etttgaggte aaetgaeaaa
                                                                     120
aactccaagt tgactaggca gtgctcgcct aacggtggat cttgttctcg tcattttcac
                                                                     180
tgctgcagcc tctattgcaa taaaaatact ggcgtatgta ttgcaaccta atacccgtgt
                                                                     240
qtqqtcatqa accactcaat accctctcct ctqqaqqctt caqaqqaact qcattqaaat
                                                                     300
                                                                     330
aaaactgcat tgcnttgacc aaaaaaaaaa
<210>
       214
<211>
       76
<212> PRT
<213> Conus pulicarius
<400> 214
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Lys His
                                25
```

```
Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
                            40
Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
<210>
       215
<211>
       30
<212>
       PRT
<213>
      Conus pulicarius
<220>
<221>
      PEPTIDE
       (1)..(30)
<222>
      Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 is Pro or H
       yp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Ty
<400> 215
Xaa Cys Ser Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
Ser Leu Xaa Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
       216
<210>
       282
<211>
<212>
       DNA
<213>
       Conus purpurascens
<400> 216
                                                                       60
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgttcc tgacggcctg tcaactcatc
acagctgatg actocagacg tacgcagaag catogtgood tgaggtogad caccaaaggo
                                                                       120
gccacgtcga atcgcccctg caagacaccc ggacgaaaat gttttccgca tcagaaggac
                                                                       180
tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta
                                                                       240
                                                                       282
tccttttctg cctgagtctc cttacctgag agtggtcatg aa
       217
<210>
       72
<211>
 <212>
      PRT
 <213> Conus purpurascens
 <400> 217
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
 Ala Leu Arg Ser Thr Thr Lys Gly Ala Thr Ser Asn Arg Pro Cys Lys
                             40
 Thr Pro Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
 Ala Cys Ile Ile Thr Ile Cys Pro
```

```
<210> 218
<211> 27
<212> PRT
<213> Conus purpurascens
<220>
<221> PEPTIDE
<222>
       (1)..(27)
      Xaa at residue 1, 5, 11 and 27 is Pro or Hyp
<400> 218
Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa
<210>
       219
<211>
       340
<212>
       DNA
<213> Conus purpurascens
<400> 219
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                       60
acqqcctqtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
                                                                     120
aggtcgacca ccaaactctt cacgtcgaaa agctgcaagc ttcccggagc atattgtaat
                                                                      180
                                                                      240
qcaqaaqatt atqactqctq ccttagatqc aaagttggag gtacatgtgg ctgatccagt
                                                                      300
qcctqatctt ccccttctq tqctctatcc ttttctqcct gagtcctcct tacctaagag
tggtcatgaa ccactcatca ccttctcctc tggaggcttc
                                                                      340
<210>
       220
<211> 71
<212> PRT
<213> Conus purpurascens
<400> 220
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu
Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys
Lys Val Gly Gly Thr Cys Gly 65 70
       221
<210>
<211>
       26
<212>
       PRT
<213> Conus purpurascens
<220>
<221> PEPTIDE
```

```
<222> (1)..(26)
<223> Xaa at residue 12 is Glu or gamma-carboxy Glu; Xaa at residue 5 i
      s Pro or Hyp; Xaa at residue 8 and 14 is Tyr, 125I-Tyr, mono-iodo
       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 221
Ser Cys Lys Leu Xaa Gly Ala Xaa Cys Asn Ala Xaa Asp Xaa Asp Cys
Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
<210>
      222
<211>
      317
<212>
      DNA
<213>
      Conus purpurascens
<400> 222
atqaaactqa cgtgtgtggt gatcgtcgcc gtgctgttcc tgacggcctg tcaactcatc
                                                                      60
acagetgatg actocagacg tacgeagaag categtgeec tgaggtegae caceaaacge
                                                                     120
gccacgtcga atcgcccctg caagaaaacc ggacgaaaat gttttccgca tcagaaggac
                                                                     180
tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta
                                                                     240
tecttttetq cetqaqteet cettacetqa qaqtqqteat qaaceactea teacettete
                                                                     300
                                                                     317
ctctggaggc ttcagag
<210> 223
<211>
      72
<212> PRT
<213> Conus purpurascens
<400> 223
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
                            40
Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
Ala Cys Ile Ile Thr Ile Cys Pro
                    70
<210>
      224
<211> 27
<212> PRT
<213> Conus purpurascens
<220>
<221>
      PEPTIDE
<222>
       (1)..(27)
<223>
      Xaa at residue 1, 11 and 27 is Pro or Hyp
<400> 224
Xaa Cys Lys Lys Thr Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
```

```
Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa
<210>
       225
<211>
       328
<212>
       DNA
<213> Conus radiatus
<400> 225
gctgatgcct gatcttcatc gttcttccct gtctcctttg gcatcaccaa aaccatcatc
                                                                      60
aaaatqaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc
                                                                     120
                                                                     180
atcacagetg atgactecag aggtatgeag aaacateatg eeetggggte gateageagt
ctctttaagt cgacccgtca tggctgcaaa cccctcaaac gtcgttgttt caatgataaa
                                                                     240
                                                                     300
qaatqctqca qcaaattttq caattcagtc cgaaaqcagt gtggataaat ggctaaaaaa
                                                                     328
ctgaataaaa gccgcattgc aaaaaaaa
<210> 226
<211> 74
<212> PRT
<213> Conus radiatus
<400> 226
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys
        35
Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
Phe Cys Asn Ser Val Arg Lys Gln Cys Gly
<210> 227
<211> 28
<212> PRT
<213> Conus radiatus
<220>
<221>
      PEPTIDE
<222>
      (1)..(28)
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 i
       s Pro or Hy
<400> 227
His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
<210> 228
<211>
       250
<212> DNA
<213> Conus radiatus
```

<400> 228 gaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc 60 atcacagctg atgactccag aggtatgcag aaacatcatg ccctggggtc gatcagcagt 120 ctetttaagt cgacccgtcg tggctgcaaa cccctcaaac gtcgttgttt caatgataaa 180 240 gaatgctgca gcaaattttg caattcagtc cgaaaccagt gtggataaat ggctaaaaac tgaataaaag 250 <210> 229 <211> 74 <212> PRT <213> Conus radiatus <400> 229 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys Gly <210> 230 <211> 28 <212> PRT <213> Conus radiatus <220> <221> PEPTIDE <222> <223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 i s Pro or Hy <400> 230 Arg Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys <210> 231 <211> 435 <212> DNA <213> Conus radiatus <400> 231 ggaattccgc ttgcacggcg aacctgactt catctttctt ccctgcctcc tttggcatca 60 ccaaaaccat catcaaaatg aaactgacgt gtgtggtgat cgtcgccgtg ctggtcctga 120 cggcctgtca actcatcaca gctgatgact ccagaggtat gcagaagcat catgccctga 180 ggtcgatcac caaactctcc ctgtcgactc gctgcaaacc tcccggatca ccatgtagag 240

tttcttcgta taactgctgc tcttcttgca aatcatacaa caagaaatgt ggctgaactt

coccttotgt gototatoot tttootgood gagtootoda tacotgagag tagtoatgaa	360
ccactgatta cctactcctc tggagggcct cagaggagct actttgaaat aaaagcccgc	420
attgcaaaaa aaaaa	435
<210> 232 <211> 72 <212> PRT <213> Conus radiatus	
<400> 232	
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala 1 5 10 15	
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His 20 25 30	
Ala Leu Arg Ser Ile Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Pro 35 40 45	
Pro Gly Ser Pro Cys Arg Val Ser Ser Tyr Asn Cys Cys Ser Ser Cys 50 55	
Lys Ser Tyr Asn Lys Lys Cys Gly 65 70	
<210> 233 <211> 27 <212> PRT <213> Conus radiatus	
<220> <221> PEPTIDE <222> (1)(27) <223> Xaa at residue 3, 4 and 7 is Pro or Hyp; Xaa at residue 13 and is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or phospho-Ty	
<400> 233 Cys Lys Xaa Xaa Gly Ser Xaa Cys Arg Val Ser Ser Xaa Asn Cys Cys 1 5 10 15	
Ser Ser Cys Lys Ser Xaa Asn Lys Lys Cys Gly 20 25	
<210> 234 <211> 392 <212> DNA <213> Conus rattus	
<400> 234 ggatccatga aactgacgtg catggtgatc atcgccgtgc tgttcctgac agcctgtcaa	60
ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct	120
gacaaacaca tcaggttgac caagcgttgc aatgctcgca atgatggttg cagtcaacat	180
tetcaatget geagtggate ttgcaataag actgeaggeg tatgtetgta aagetggtet 2	240
geogtetgat attecettte tgtgetttat eetettttge etgagteate catacetgtg	300
aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat	360

aaagccacat tgcaaaaaaa aaaaaaaaaa aa									
<210> 235 <211> 74 <212> PRT <213> Conus rattus									
<400> 235 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala 1 5 10 15									
Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro 20 25 30									
Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys 35 40 45									
Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly 50 60									
Ser Cys Asn Lys Thr Ala Gly Val Cys Leu 65 70									
<210> 236 <211> 27 <212> PRT <213> Conus rattus									
<400> 236 Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser 1 5 10 15									
Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu 20 25									
<210> 237 <211> 395 <212> DNA <213> Conus rattus									
<400> 237 ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa	60								
ctcgatgcag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct	120								
gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat	180								
cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct	240								
gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg	300								
aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat	360								
aaagccacat tgcaacgaaa aaaaaaaaa aaaaa	395								
<210> 238 <211> 74 <212> PRT <213> Conus rattus									
<400> 238 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala 1 5 10 15									

Cys Gln Leu Asp Ala Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys 35 40 45	
Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly 50 60	
Ser Cys Asn Lys Thr Ala Gly Val Cys Leu 65 70	
<210> 239 <211> 27 <212> PRT <213> Conus rattus	
<220> <221> PEPTIDE <222> (1)(27) <223> Xaa at residue 12 is Pro or Hyp	
<pre><400> 239 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser 1</pre>	
Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu 20 25	
<210> 240 <211> 390 <212> DNA <213> Conus rattus	
<400> 240 ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa	60
ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct	120
gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat	180
cctcaatgct gcagtggatc ttgcaataag actttgggcg tatgtctgta aagctggtct	240
geogtetgat attecettte tgtgetttat estettttge etgagteate catacetgtg	300
aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat	360
aaagccacat tgaaaaaaaa aaaaaaaaaaa	390
<210> 241 <211> 74 <212> PRT <213> Conus rattus	
<400> 241 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala 1 5 10 15	
Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro 20 25 30	
Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys 35 40 45	
Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly	

```
Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
65
<210> 242
<211> 27
<212> PRT
<213> Conus rattus
<220>
<221>
       PEPTIDE
<222>
       (1)..(27)
<223> Xaa at residue 12 is Pro or Hyp
<400> 242
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser
Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
                                25
<210>
       243
<211>
       379
<212> DNA
<213> Conus stercusmuscarum
<400> 243
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                      60
acqqcctqtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg
                                                                     120
                                                                     180
aggtcgaaga ccaaactctc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca
aggettatgt atgactgetg cageggttet tgcagegget acacaggtag atgtggetga
                                                                      240
                                                                     300
tecagegeet gatetteece ettetgtget etateetttt etgeetgggt eeteettace
tgagagtggt catgaaccac tcatcaccta ctcctctgga ggcctcagag gagttacaat
                                                                      360
                                                                      379
gaaataaaag ccgcattgc
<210>
       244
<211>
       73
<212>
       PRT
<213> Conus stercusmuscarum
<400> 244
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
                                                    30
                                25
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser
Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser
                        55
Cys Ser Gly Tyr Thr Gly Arg Cys Gly
<210> 245
<211> 27
<212> PRT
```

```
<213> Conus stercusmuscarum
<220>
<221>
      PEPTIDE
<222>
       (1)..(27)
<223>
      Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo
       -Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 245
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys
Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys
            2.0
<210> 246
<211>
      35
      PRT
<212>
<213>
      Conus stercusmuscarum
<220>
<221>
      PEPTIDE
<222>
       (1)..(35)
      Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
         is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
       -phospho-Ty
<400> 246
Thr Thr Ser Cys Met Gln Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg
Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
Xaa Ser Asn
        35
<210>
       247
<211>
       380
<212>
       DNA
<213>
       Conus stercusmuscarum
<400> 247
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                       60
acquectgtc aucteateue agetgatgae tecagaggta egeaggagea tegtgeeetg
                                                                      120
aggtcgaaga ccaaactete catgttaact ttgcgctgcg catcttacgg aaaacettgt
                                                                      180
ggtattgaca acgactgctg caatgcatgc gatccagcca gaaatatatg tacgtagctg
                                                                      240
atcoggogto tgatottoco cottotgtgo totatocttt totgcotgag toctcottac
                                                                      300
ctgagagtgg tcatgaacca ctcatcatct actctcctgg aggcctcaga ggagctacaa
                                                                      360
tgaaataaaa gccgcattgc
                                                                      380
<210>
       248
<211>
       72
      PRT
<212>
<213>
      Conus stercusmuscarum
<400> 248
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Thr
                                    10
```

```
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
Asp Pro Ala Arg Asn Ile Cys Thr
      249
<210>
<211>
       26
<212>
      PRT
<213>
      Conus stercusmuscarum
<220>
<221> PEPTIDE
<222>
       (1)..(26)
       Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue4 is Tyr, 1
       251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 249
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
<210>
       250
<211>
       388
<212>
       DNA
      Conus stercusmuscarum
<213>
<400> 250
ggatccatga aactgacgtg tgtggtgatt gtcgccgtgc tgctcctgac ggcctgtcaa
                                                                      60
ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtcgaagacc
                                                                      120
aaactctcca tgttaacttt gegetgegta tettaeggaa aacettgtgg tattgacaae
                                                                      180
qactqctqca atqcatqcqa tccaqccaqa aatatatgta cgtaqctgat ccggcgtctg
                                                                      240
                                                                      300
atcttccccc ttctqtqctc tatccttttc tgcctqgqtc ctccttacct gagagtqgtc
atgaaccact catcacctac tcctctggag gcctcagagg agttacaatg aaataaaagc
                                                                      360
                                                                      388
cqcattqcaa aaaaaaaaaa aaaaaaaa
<210>
       251
<211>
       72
<212>
      PRT
<213> Conus stercusmuscarum
<400> 251
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
```

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val

	35					4 U					45				
Ser Typ 50	Gly	Lys	Pro	Cys	Gly 55	Ile	Asp	Asn .	Asp	Cys 60	Cys .	Asn	Ala	Cys	
Asp Pro) Ala	Arg		Ile 70	Cys	Thr									
<210> <211> <212> <213>	252 26 PRT Conus	s ste	ercus	musc	arum	ı									
<220> <221> <222> <223>	PEPT: (1). Xaa a 25I-	.(26) at re	sidu	e 7 -iod	and lo-Ty	20 i	s Pr di-io	ro or odo-T	Hyp yr,); Xa O-su	a at llpho	res -Tyr	sidue r or	4 is O-phos	Tyr, 1 pho-Ty
<400> Cys Va 1	252 l Ser	Xaa	Gly 5	Lys	Xaa	Cys	Gly	Ile 10	Asp	Asn	Asp	Cys	Cys 15	Asn	
Ala Cy	s Asp	Xaa 20	Ala	Arg	Asn	Ile	Cys 25	Thr							
<210> <211> <212> <213>		s sti	riatu	ıs											
<400> accaaa	253 acca	tcato	caaaa	at ga	aact	gac	g tgt	igtgg	ıtga	tcgt	cgcc	gt 🤅	gatgo	ctcctg	60
acggcc	tgtc	aacto	catca	ac aç	gctga	atgad	c to	cagag	gta	cgca	agaag	ıca t	tcgtt	ccctg	120
aggtcg	acca	ccaaa	agtct	cc ca	aaggo	cgact	t ga	ctgca	ittg	aago	ccgga	aa t	ttatt	gcgga	180
cctact	gtta	tgaaa	aatct	g ct	geg	gctti	t tg	cagto	ccat	acaç	gcaaa	at a	atgta	atgaac	240
tatccc	aaaa	attg	atctt	ic c	ccc										264
<210><211><211><212><213>		ıs st:	riatı	ıs											
<400> Met Ly 1	254 s Leu	Thr	Cys 5	Val	Val	Ile	Val	Ala 10	Val	Leu	Leu	Leu	Thr 15	Ala	
Cys Gl	n Leu	ille 20	Thr	Ala	Asp	Asp	Ser 25	Arg	Gly	Thr	Gln	Lys 30	His	Arg	
Ser Le	u Arg 35	ßer	Thr	Thr	Lys	Val 40	Ser	Lys	Ala	Thr	Asp 45	Cys	Ile	Glu	
Ala Gl 50		Tyr	Cys	Gly	Pro 55	Thr	Val	Met	Lys	Ile 60	Cys	Cys	Gly	Phe	
Cys Se	er Pro) Tyr	Ser	Lys 70	Ile	Cys	Met	Asn	Tyr 75	Pro	Lys	Asn			

```
<210> 255
<211>
       36
      PRT
<212>
<213>
      Conus striatus
<220>
<221>
      PEPTIDE
<222>
      (1)..(36)
      Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
       25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125
       I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 255
Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
Xaa Xaa Lys Asn
        35
<210>
       256
      233
<211>
<212>
      DNA
<213>
      Conus striatus
       256
<400>
gtcgactcgc tgcaagctta aaggacaatc atgtcgtagg actatgtatg actgctgcag
                                                                       60
cggttcttgc ggcaggagag gtaaatgtgg ctgatccagc gcctgatctc cccccttctg
                                                                      120
tgctctatcc ttttctgcct gggtcctcct tacctgagag tggtcatgaa ccactcatca
                                                                      180
cctactcctc tggaggcctc agaggagcta caatgaaata aaagccgcat tgc
                                                                      233
<210>
       257
<211>
       30
<212>
      PRT
<213>
      Conus striatus
<400> 257
Ser Thr Arg Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr
Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly
<210>
      258
<211> 26
<212> PRT
<213> Conus striatus
<220>
<221>
       PEPTIDE
<222>
      (1)..(26)
      Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 258
Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys
Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys 20 25
```

```
<210> 259
<211>
       310
       DNA
<212>
<213> Conus striatus
<400> 259
                                                                       60
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
acqqcctqtc aactcatcac aqctgatgac tccagaggta cgcagaagca tcgtgccctg
                                                                       120
                                                                       180
aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt
aggattgcgt ataactgctg caccggttct tgcagatcag gtaaatgcgg ctgatccagc
                                                                      240
gcctgatctt cccccttctg tgctctatcc tttctgcctg agtcctctta cctgagagtg
                                                                       300
                                                                       310
gtcatgaacc
<210>
       260
<211>
      71
<212> PRT
<213> Conus striatus
<400> 260
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
Cys Arg Ser Gly Lys Cys Gly
<210> 261
<211> 25
<212> PRT
<213> Conus striatus
<220>
<221>
      PEPTIDE
<222>
       (1)..(25)
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 261
Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210>
       262
<211>
       256
<212>
      DNA
<213> Conus striatus
<400> 262
```

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
aggtcggaca ccaaactctc catgttaact ttgcgctgcg aatcttacgg aaaaccttgt 180
ggtatttaca acgactgctg caatgcatgc gatccagcca aaaagacatg tacgtagctg 240
atccggcgtc tgatct 256
<210> 263 <211> 72 <212> PRT <213> Conus striatus
<400> 263 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala 1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg 20 25 30
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu 35 40 45
Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys 50 55 60
Asp Pro Ala Lys Lys Thr Cys Thr 65 70
<210> 264 <211> 26 <212> PRT <213> Conus striatus
<pre><220> <221> PEPTIDE <222> (1)(26) <223> Xaa at residue 2 is Glu or gamma-carboxy Glu; Xaa at residue 7 an</pre>
<400> 264 Cys Xaa Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn 1 5 10 15
Ala Cys Asp Xaa Ala Lys Lys Thr Cys Thr 20 25
<210> 265 <211> 229 <212> DNA <213> Conus striatus
<400> 265 tctaggtcct ccggcagccc ctgtggtgtt actagtatat gctgtggtag atgctatagg 60
ggtaaatgta cgtagctcat cgggcgtctg atcttccccc ttctgtgctc catccttttc 120
tgcctgagtc ctccttacct gagagtggtc gtgaaccact catcgcctac tcctctggag 180
gcttcagagg ggctacacta aaataaaagc tatattgcaa tgaaaaaaa 229

```
<210>
       266
<211>
       24
       PRT
<212>
<213>
      Conus striatus
<400> 266
Cys Arg Ser Ser Gly Ser Pro Cys Gly Val Thr Ser Ile Cys Cys Gly
                                     10
Arg Cys Tyr Arg Gly Lys Cys Thr
            20
<210>
       267
<211>
       24
<212>
      PRT
<213>
      Conus striatus
<220>
<221>
      PEPTIDE
<222>
      (1)..(24)
      Xaa at residue 7 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Ty
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 267
Cys Arg Ser Ser Gly Ser Xaa Cys Gly Val Thr Ser Ile Cys Cys Gly
                                    10
Arg Cys Xaa Arg Gly Lys Cys Thr
            20
<210>
       268
<211>
       26
<212>
      PRT
<213>
      Conus striatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(26)
<223>
      Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 268
Cys Lys Leu Lys Gly Gln Ser Cys Arg Lys Thr Ser Xaa Asp Cys Cys
                                    10
Ser Gly Ser Cys Gly Arg Ser Gly Lys Cys
<210>
       269
<211>
       292
<212>
      DNA
<213>
      Conus striolatus
<400> 269
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgtctt gctgctcctg
                                                                       60
acgacctgtc gtctcatcac agctgatgac tccagaggta cgcagaagca tcgttccctq
                                                                      120
aggtcgacta ctaaagtctc catgtcgact cgctgcaagg gtaaaggagc atcatgtctt
                                                                      180
aggactgcgt atgactgctg caccggttct tgcaacagag gtagatgtgg ctgatccagc
                                                                      240
gtctgatctt cccccttctg tgctctatcc ttttctgctt gagtcctcct ta
                                                                      292
```

```
<210> 270
      71
<211>
<212> PRT
<213> Conus striolatus
<400> 270
Met Lys Leu Thr Cys Val Val Ile Val Val Leu Leu Leu Thr Thr
Cys Arg Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
Ser Leu Arg Ser Thr Thr Lys Val Ser Met Ser Thr Arg Cys Lys Gly
Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys Thr Gly Ser
Cys Asn Arg Gly Arg Cys Gly
<210> 271
<211> 25
<212>
      PRT
<213> Conus striolatus
<220>
<221> PEPTIDE
<222>
      (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 271
Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Xaa Asp Cys Cys
                                    10
                                                        15
Thr Gly Ser Cys Asn Arg Gly Arg Cys
<210>
       272
<211>
       259
<212>
       DNA
<213> Conus striolatus
<400> 272
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgctgacg
                                                                      60
gcgtgtcaac tcatcacagc tgaggactcc agaggtacac agaagcatcg taccctgagg
                                                                     120
tegacegtea gaegeteeaa gteegagttg actaegagat geaggeette aggateeaae
                                                                     180
tgtggtaata ttagtatctg ctgtggtaga tgcgttaaca gaagatgtac gtagctcatc
                                                                     240
gggcgtctga tctttcccc
                                                                     259
<210>
       273
<211>
       71
<212>
       PRT
<213> Conus striolatus
<400> 273
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys
Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg Thr
```

11
511
1-1
TI.
32
4.
<u>L</u>

	20	25	30	
Leu Arg Ser 35	Thr Val Arg Arg	Ser Lys Ser G 40	lu Leu Thr Thr 45	Arg Cys
Arg Pro Ser 50	Gly Ser Asn Cys 55	Gly Asn Ile S	Ser Ile Cys Cys 60	Gly Arg
Cys Val Asn 65	Arg Arg Cys Thr 70			
<210> 274 <211> 24 <212> PRT <213> Conu	s striolatus			
	IDE .(24) at residue 3 is 1	Pro or Hyp		
<400> 274 Cys Arg Xaa 1	Ser Gly Ser Asn 5	Cys Gly Asn 1	Ile Ser Ile Cys	Cys Gly 15
Arg Cys Val	Asn Arg Arg Cys 20	Thr		
<210> 275 <211> 280 <212> DNA <213> Conu	s striolatus			
<400> 275 accaaaacca	tcatcaaaat gaaac	tgacg tgtgtgg	tga tegtegeegt	tctgttcctg 60
acggcgtgtc	aactcatcac agctg	jaggac tccagag	gta cacagaagca	tcgttccctg 120
aggtcgacta	ccaaagtctc caagt	cgact agctgcat	tga aagccgggtc	ttattgcgtc 180
gctactacga	gaatctgctg cggtt	attgc gcttatt:	tcg gcaaaatatg	tattgactat 240
cccaaaaact	gatetteece etaet	gtgct ctatcct	ttt	280
<210> 276 <211> 77 <212> PRT <213> Cont	ns striolatus			
<400> 276 Met Lys Let 1	ı Thr Cys Va l Val 5	l Ile Val Ala 1	Val Leu Phe Leu	Thr Ala 15
Cys Gln Let	ı Ile Thr Ala Glu 20	ı Asp Ser Arg 25	Gly Thr Gln Lys 30	s His Arg
Ser Leu Aro	g Ser Thr Thr Lys	s Val Ser Lys 40	Ser Thr Ser Cys 45	s Met Lys
Ala G1y Se: 50	r Tyr Cys Val Ala 55	a Thr Thr Arg	Ile Cys Cys Gly 60	y Tyr Cys
Ala Tyr Pho	e Gly Lys Ile Cys 70	s Ile Asp Tyr	Pro Lys Asn 75	

```
<210> 277
<211>
      35
<212>
     PRT
<213> Conus striolatus
<220>
      PEPTIDE
<221>
<222>
       (1)..(35)
      Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
        is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
       phospho-Ty
<400> 277
Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Asp Xaa
Xaa Lys Asn
        35
<210>
       278
<211>
       1.74
<212>
       DNA
<213>
       Conus textile
<400> 278
gttgactcgg tactgcacgc ctcatggagg acattgtggt tatcataatg actgctgcag
                                                                       60
tcatcaatgc aatataaaca gaaataaatg tgagtagctg atctggcatc tgatctgtgc
                                                                      120
                                                                      174
tcqtccttac ctqaqaqtqq tcatqaacca ctcatcacct actcctctgq aggc
<210>
       279
<211>
      31
<212>
      PRT
<213> Conus textile
<400> 279
Leu Thr Arg Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn
Asp Cys Cys Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
<210>
       280
<211>
       28
<212>
       PRT
<213>
      Conus textile
<220>
<221>
       PEPTIDE
<222>
       (1)..(28)
       Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 i
       s Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo
       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 280
Xaa Cys Thr Xaa His Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
            20
```

```
<210> 281
<211> 28
<212> PRT
<213> Conus textile
<220>
<221> PEPTIDE
<222>
      (1)..(28)
      Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 i
<223>
       s Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo
       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 281
Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
<210>
       282
<211>
      379
<212> DNA
<213> Conus tulipa
<400> 282
                                                                      60
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
acggcctgtc agctcatcac agctctgcac tccagaggta cgcagaagca tcgtgccctg
                                                                      120
gggcggacca ccaaactcac cttgtcgact cgctgcaaat cacccggatc tccatgttca
                                                                      180
ccgactagtt ataattgctg ctggtcttgc agtccataca gaaaaaaatg taggggctaa
                                                                      240
                                                                      300
tocagogoot gattttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc
tgaaagtggt catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt
                                                                      360
                                                                      379
gaaataaaag ccgcattgc
<210>
       283
<211>
       73
       PRT
<212>
<213>
       Conus tulipa
<400> 283
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Gly Arg Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
 Pro Gly Ser Pro Cys Ser Pro Thr Ser Tyr Asn Cys Cys Trp Ser Cys
Ser Pro Tyr Arg Lys Lys Cys Arg Gly
<210> 284
<211>
       27
<212>
       PRT
 <213> Conus tulipa
```

```
<220>
       PEPTIDE
<221>
<222>
      (1)..(27)
      Xaa at residue 3, 7, 10 and 21 is Pro or Hyp; Xaa at residue 17 i
       s Trp or Bromo Trp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mo
       no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 284
Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
                                    10
Xaa Ser Cys Ser Xaa Xaa Arg Lys Lys Cys Arg
<210> 285
<211>
      379
<212>
      DNA
<213> Conus tulipa
<400> 285
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                       60
acqqcctqtc agctcatcac agctctqcac tccaqagqta cqcaqaaqca tcqtqccctq
                                                                      120
gggtcgacca ccaaactcac cttgtcgact cgctgcttgt cacccggatc ttcatgttca
                                                                      180
ccqactaqtt ataattqctq cagqtcttqc aatccataca gcagaaaatg taggggctaa
                                                                      240
tocagegeet gatetteece ettetgtget etatteettt etgeetgagt eeteettace
                                                                      300
tqaaaqtqqt catqaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt
                                                                      360
                                                                      379
gaaataaaag ccgcattgc
<210>
       286
       73
<211>
<212>
      PRT
<213> Conus tulipa
<400> 286
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg
Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser
Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
    50
                        55
                                            60
Asn Pro Tyr Ser Arg Lys Cys Arg Gly
<210>
       287
<211>
       27
<212>
       PRT
<213>
      Conus tulipa
<220>
<221>
       PEPTIDE
<222>
       (1)..(27)
<223>
       Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and
```

22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or

O-phospho-Ty

<400> 290

<400> 287 Cys Leu Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys Arg Ser Cys Asn Xaa Xaa Ser Arg Lys Cys Arg <210> 288 <211> 401 <212> DNA <213> Conus viola <400> 288 60 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg acggcctgtc agctcattac agctgatgac tccagaggta cgcagttgca tcgtgccctg 120 aggaaggcca ccaaactccc cgtgtcgact cgctgcatta ctttaggaac acgatgtaag 180 gttccgagtc aatgctgcag atcttcttgc aagaacggtc gttgtgctcc atcccctgaa 240 gaatggtaaa tgtggctgat ccagcgcctg atcttccccc ttctgactgt ctccgacctt 300 360 ttctqcctqa qtcctcctta cctgagaggt gtcatgaacc actcatcacc tactcccctg gaagcttcag aggagctaca ttgaaataaa agccgcattg c 401 <210> 289 <211> 76 <212> PRT <213> Conus viola <400> 289 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala 10 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Leu His Arg Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp 70 <210> 290 <211> 31 <212> PRT <213> Conus viola <220> <221> PEPTIDE <222> (1)..(31)Xaa at residue 29 and 30 is Glu or gamma-carboxy Glu; Xaa at resi due 11, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Brom o Tr

Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Xaa Ser Gln Cys Cys Arg

1	5		10	15	
Ser Ser Cys I	Lys Asn Gly 2 20	Arg Cys Ala 25	Xaa Ser Xaa	Xaa Xaa Xa 30	a
<210> 291 <211> 372 <212> DNA <213> Conus	viola				
<400> 291 accaaaacca to	catcaaaat ga	aactgacg tg	gtggtga tcg	tegeegt get	gctcctg 60
acggcctgtc ac	gctcattat ag	ctggggac tc	cagaggta cgc	agttgca tcg	tgccctg 120
aggaaggcca co	caaactctc cg	tgtcgact cg	ctgcaaga gta	gaggatc atc	atgtcgt 180
aggacttcgt at	tgactgctg ca	cgggttct tg	cagaaatg gta	aatgtgg ctg	atccagc 240
gcctgatctt co	secettetg tg	ctccatcc tt	tctgcct gag	tcctcct tac	ctgagag 300
tgggcatgaa co	cactcatca cc	tactccct gga	aagcttca gag	gagctac att	gaaataa 360
aagccgcatt go	C				372
<210> 292 <211> 71 <212> PRT <213> Conus	viola				
<400> 292 Met Lys Leu 7	Thr Cys Val ' 5	Val Ile Val	Ala Val Leu 10	Leu Leu Th 15	r Ala
Cys Gln Leu	Ile Ile Ala (20	Gly Asp Ser 25	Arg Gly Thr	Gln Leu Hi 30	s Arg
Ala Leu Arg I	Lys Ala Thr	Lys Leu Ser 40	Val Ser Thr	Arg Cys Ly 45	s Ser
Arg Gly Ser S		Arg Thr Ser 55	Tyr Asp Cys	Cys Thr Gl	y Ser
Cys Arg Asn (Gly Lys Cys (Gly			
<210> 293 <211> 25 <212> PRT <213> Conus	viola				
	(25)		5I-Tyr, mono	-iodo-Tyr,	di-iodo-Tyr, C
<400> 293 Cys Lys Ser A	Arg Gly Ser a	Ser Cys Arg	Arg Thr Ser	Xaa Asp Cy 15	s Cys
Thr Gly Ser (Gly Lys Cys 25		10	

<210> 294 <211> 380 <212> DNA <213> Conus viola	
<400> 294 accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg	60
acggcctgtc agctcattac agctgaagac tccagaggta cgcatgagca tcttgccctg	120
aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccagatc ttattgcgga	180
cctgctacta cgaaaatctg ctgcgatttt tgcagtccat tcagcgatag atgtatgaac	240
aatcccaaca attgatcttc ccccttgtgt gctccatctt ttctgcctga gtcctcctta	300
cctgagagtg gtcatgaacc actcatcacc tactcctctg gaggcttcag aggagttaca	360
ttgaaataaa agccgcatgc	380
<210> 295 <211> 78 <212> PRT <213> Conus viola	
<400> 295 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala 1 5 10 15	
Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu 20 25 30	
Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu 35 40 45	
Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe 50 60	
Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn 65 70 75	
<210> 296 <211> 36 <212> PRT <213> Conus viola	
<220> <221> PEPTIDE <222> (1)(36) <223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, -iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty	13, mono
<400> 296 Ser Thr Ser Cys Met Xaa Ala Arg Ser Xaa Cys Gly Xaa Ala Thr Thr 1 5 10 15	
Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn 20 25 30	
Asn Xaa Asn Asn 35	
<210> 297 <211> 373	

```
<212> DNA
<213> Conus viola
<400> 297
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg
                                                                       60
                                                                      120
acggcctgtc agctcattac agctgaggac tccagaggta cgcagttgca tcgtgccctg
aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc catatgtata
                                                                      180
aggattgcgt ataactgctg caagtattct tgcggaaatg gtaaatgtgg ctgatccagc
                                                                      240
                                                                      300
quetquetett coccettgtg tgetecated tittletged tgagtdeted ttacetgaga
                                                                      360
gtggtcatga accactcatc acctactcct ctggaggctt cagaggagct acattgaaat
                                                                      373
aaaagccgca tgc
<210>
      298
<211>
      PRT
<212>
<213> Conus viola
<400> 298
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
                        55
                                             60
Cys Gly Asn Gly Lys Cys Gly
<210>
       299
<211>
       25
<212> PRT
<213> Conus viola
<220>
       PEPTIDE
<221>
<222>
       (1)..(25)
       Xaa at residue 3 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
<400> 299
Cys Lys Gly Xaa Gly Ala Ile Cys Ile Arg Ile Ala Xaa Asn Cys Cys
Lys Xaa Ser Cys Gly Asn Gly Lys Cys
<210>
       300
<211>
       353
<212>
       DNA
<213>
       Conus viola
<400> 300
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttcctg
```

acggcctgtc	aattcato	cac agc	tgatgac	tcc	agaa	.gta	cgca	gaag	ıca ·	tcgtg	jccctg	120
aggtcgacca	ccaaaca	ctt tat	gttgact	tgg	tact	gca	cgcc	ttat	gg (aggac	cattgt	180
ggttattata	atgactgo	ctg cag	tcatcaa	tgc	aata	taa	acag	aaat	aa	atgto	gagtag	240
ctgatccggc	atctgate	ctg tgc	tcgccct	aac	ctga	gag	tggt	cato	jaa -	ccact	catca	300
tctactcctc	tggaggc	tc aga	ggagcta	cat	ggaa	ata	aaag	ccgc	at	tgc		353
<210> 301 <211> 73 <212> PRT <213> Con												
<400> 301 Met Lys Le 1		s Val V	al Ile	Val	Ala 10	Val	Leu	Phe	Leu	Thr 15	Ala	
Cys Gln Ph	e Ile Th	r Ala A	sp Asp	Ser 25	Arg	Ser	Thr	Gln	Lys 30	His	Arg	
Ala Leu Ar	_	r Thr L	ys His 40	Phe	Met	Leu	Thr	Trp 45	Tyr	Cys	Thr	
Pro Tyr Gl 50	y Gly Hi	s Cys G 5		Tyr	Asn	Asp	Cys 60	Cys	Ser	His	Gln	
Cys Asn Il 65	e Asn Ar	g Asn L 70	ys Cys	Glu								
<210> 302 <211> 28 <212> PRI <213> Cor												
<222> (1) <223> Xaa s H	PTIDE(28) at resi Pro or Hy iodo-Tyr	p; Xaa	at resi	idue	1, 5	5, 13	l and	12	is	Tyr,	125I-Ty	e 4 i
<400> 302 Xaa Cys Th 1	? nr Xaa Xa 5	a Gly G	ly His	Cys	Gly 10	Xaa	Xaa	Asn	Asp	Cys 15	Cys	
Ser His G	n Cys As 20	n Ile A	sn Arg	Asn 25	Lys	Cys	Xaa					
<210> 303 <211> 294 <212> DNA <213> Cor	ļ	arius										
<400> 303 ggatccatga		gtg cgt	.ggtgat	t ato	cgcc	gtgc	tgti	tcct	gac	ggcc	tgtcaa	60
ctcattacaç	g ctgagac	tta ctc	cagaggt	t aaq	gcaga	atgc	acc	gtgc	tct	gagg	tcaact	120
gacaaaaact	ccaagtt	gac cag	ggaatg	c aca	acct	ccag	atg	gagc	ttg	tggt	ttacct	180
acacactgct	gcgggtt	ttg cga	tatggca	a aad	caaca	agat	gtc	tgta	aag	cgtc	tgatat	240

```
teceettetg tgetetatee tetttggeet gagteateea taeetgtget egag
                                                                     294
<210> 304
<211> 73
<212> PRT
<213> Conus pulicarius
<400> 304
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Glu Cys
Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
Cys Asp Met Ala Asn Asn Arg Cys Leu
<210> 305
<211> 27
<212> PRT
<213> Conus pulicarius
<220>
<221>
       PEPTIDE
<222>
       (1)..(27)
<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5
        and 12 is Pro or Hy
<400> 305
Xaa Cys Thr Xaa Xaa Asp Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
<210>
       306
 <211>
       294
 <212>
       DNA
 <213> Conus pulicarius
 <400> 306
 ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa
                                                                       60
 ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact
                                                                      120
 gacaaaaact cccagttgac cagggaatgc acacctccag gtggagcttg tggtttacct
                                                                      180
 acacactgct gcgggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat
                                                                      240
 teceettetg tgetetatee tetttggeet gagteateea taeetgtget egag
                                                                      294
 <210>
        307
        73
 <211>
 <212>
        PRT
 <213>
       Conus pulicarius
 <400> 307
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
```

```
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
                                25
            20
Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
Cys Asp Met Ala Asn Asn Arg Cys Leu
                    70
<210> 308
<211> 27
<212> PRT
<213> Conus pulicarius
<220>
<221>
      PEPTIDE
<222>
       (1)..(27)
      Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5
<223>
        and 12 is Pro or Hy
<400> 308
Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
                                    10
Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
<210>
       309
       307
<211>
<212>
      DNA
<213>
      Conus rattus
<400> 309
ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctggc agcctgtcaa
                                                                       60
cctqttacaa ctgagacttt ctccagaggt aaggagaagc gtcgtgctct gaggtcaact
                                                                      120
qacqqcaact cccqqttqac cagggcatgc acgcctgaag gtggagcctg tagtagtggg
                                                                      180
cgtcactgct gcggcttttg cgataacgtg tcccacacgt gctatggtga aacaccatct
                                                                      240
ctccactgat gtttcccctt ctgtgctcta tcttcttttg cctgagtcat ccatacctgt
                                                                      300
                                                                      307
gctcgag
<210>
       310
<211>
       80
<212>
       PRT
<213> Conus rattus
<400> 310
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Ala Ala
Cys Gln Pro Val Thr Thr Glu Thr Phe Ser Arg Gly Lys Glu Lys Arg
Arg Ala Leu Arg Ser Thr Asp Gly Asn Ser Arg Leu Thr Arg Ala Cys
                             40
```

Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys Gly Phe

50					55					60					
Cys Ası 65	o Asn	Val S		His 70	Thr	Cys	Tyr	Gly	Glu 75	Thr	Pro	Ser	Leu	His 80	
<210> <211> <212> <213>	311 34 PRT Conus	ratt	tus												
<220> <221> <222> <223>	Yaa a	(34) t res	31 i	s Pr	o or	Нур	; Xa	a at	res	sidue	e 27	is	Tyr,	1251-	at resid -Tyr, mo
<400> Ala Cy 1	311 s Thr		Xaa 5	Gly	Gly	Ala	Cys	Ser 10	Ser	Gly	Arg	His	Cys 15	Cys	
Gly Ph	e Cys	Asp 2	Asn	Val	Ser	His	Thr 25	Cys	Xaa	Gly	Xaa	Thr 30	Xaa	Ser	
Leu Hi	s														
<210> <211> <212> <213>	342 DNA	s ste	rcus	musc	arun	ı									
<220> <221> <222> <223>	(1)	(342)	nucl	Leoti	lde									
<400> agatco	312 atga a	aactg	acgt	g cg	gtggt	gato	c gto	cgcc	gtgc	tgc	tcct	gac	ggcc	tgtca:	a 60
ctcato	cacag o	ctgat	gact	C Ca	agag	gtac	g caq	ggag	catc	gtg	ccct	gag	gtcg	gacac	c 120
aaacto	ccca t	tatcg	gacto	cg ct	gca	aggg1	t aaa	agga	gcat	cat	gtca	taa	gact	atgta	t 180
gactgo	ctgca (geggt	tcct	g ca	acca	gaggi	t aga	atgt	ggct	gat	ccag	lcdc	ctga	tcttc	c 240
ccctt	ctgtg (ctcta	atcct	t ti	tctg	cctg	a gt	catc	atac	ctg	tgct	cga	gcgt	tacta	g 300
tggato	ccgag (ctcgg	gtaco	ca a	gctt	ggcg	t aa	tcat	aaaa	nc					342
<210> <211> <212> <213>		s ste	ercus	smus	caru	m									
<400> Met Ly 1	313 ys Leu	Thr	Cys 5	Val	Val	Ile	Val	Ala 10	ı Val	. Leu	ı Leı	ı Le	u Thi 15	c Ala	
Cys G	ln Leu	Ile 20	Thr	Ala	Asp	Asp	Ser 25	Arg	g Gly	7 Thr	Glı	n Gl 30	u His	s Arg	
Ala L	eu Arg 35	Ser	Asp	Thr	Lys	Leu 40	Pro	Ile	e Sei	r Thi	45	g Cy	s Ly:	s Gly	

```
Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys Ser Gly Ser
Cys Thr Arg Gly Arg Cys Gly
<210>
       314
<211>
       25
<212> PRT
<213> Conus stercusmuscarum
<220>
<221> PEPTIDE
<222>
      (1)..(25)
<223>
       Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Ty
<400> 314
Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Xaa Asp Cys Cys
                                    10
Ser Gly Ser Cys Thr Arg Gly Arg Cys
            20
<210>
       315
<211>
       33
<212> PRT
<213> Conus arenatus
<400> 315
Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr
            20
                                25
Pro
<210>
      316
<211>
      28
<212> PRT
<213> Conus arenatus
<400> 316
Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys
Ser Gly Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
            20
<210> 317
<211> 33
<212> PRT
<213> Conus arenatus
<400> 317
Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
                                    10
Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
Pro
```

```
<210> 318
<211> 33
<212> PRT
<213> Conus arenatus
<400> 318
Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
Pro
<210> 319
<211> 27
<212> PRT
<213> Conus arenatus
<400> 319
Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
                                    10
Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu
            20
<210>
       320
       28
<211>
<212> PRT
<213> Conus arenatus
<400> 320
Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys
                                    10
Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala
<210> 321
<211>
       30
<212> PRT
<213> Conus arenatus
<400> 321
Gln Cys Ser Pro Ile Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys
Ser Asn His Cys Ile Lys Pro Ile Gly Arg Cys Val Ala Thr
                                 25
<210>
       322
<211> 30
<212> PRT
<213> Conus arenatus
<400> 322
 Gln Cys Leu Pro Asn Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys
 Ser Asp His Cys Ile Lys Pro Ile Asp Arg Cys Val Ala Thr
                                 25
```

<211> 31

```
<210> 323
<211> 25
<212> PRT
<213> Conus aurisiacus
<400> 323
Cys Lys Gly Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210> 324
<211> 32
<212> PRT
<213> Conus aurisiacus
<400> 324
Cys Met Glu Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys
Gly Phe Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
<210> 325
<211> 25
<212> PRT
<213> Conus aurisiacus
<400> 325
Cys Lys Ala Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210> 326
<211> 26
<212> PRT
<213> Conus aurisiacus
 <400> 326
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
 Ala Cys Asp Pro Gly Arg Asn Ile Cys Thr
 <210> 327
 <211> 36
 <212> PRT
 <213> Conus bullatus
 <400> 327
 Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
 Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
 Asn Pro Asn Asn
         35
 <210> 328
```

```
<212> PRT
<213> Conus bullatus
<400> 328
Cys Ile Thr Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
Gly Pro Cys Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp
<210> 329
<211>
      26
<212> PRT
<213> Conus bullatus
<400> 329
Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
Thr Cys Asp Pro Ala Arg Arg Thr Cys Thr
<210> 330
<211> 25
<212> PRT
<213> Conus bullatus
<400> 330
Cys Lys Gly Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys
Lys Tyr Ser Cys Arg Asn Gly Lys Cys
<210> 331
<211> 36
<212> PRT
<213> Conus bullatus
<400> 331
Ser Thr Ser Cys Met Ala Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
Asn Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Lys
Lys Pro Asn Asn
       35
<210> 332
<211> 25
<212>
      PRT
<213> Conus bullatus
<400> 332
Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
Thr Gly Ser Cys Arg Asn Gly Arg Cys
<210> 333
<211> 25
<212> PRT
```

```
<213> Conus catus
<400> 333
Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
Thr Gly Ser Cys Arg Ser Gly Arg Cys
<210> 334
<211> 25
<212> PRT
<213> Conus catus
<400> 334
Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
Ser Gly Ser Cys Asn Arg Gly Ser Cys
<210> 335
<211> 28
<212> PRT
<213> Conus catus
<400> 335
Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
<210> 336
<211> 25
<212> PRT
<213> Conus catus
<400> 336
Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe Asn Cys Cys
Ser Gly Ser Cys Asn Arg Gly Arg Cys
<210> 337
<211> 26
<212> PRT
<213> Conus catus
<400> 337
Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
<210> 338
<211> 25
<212> PRT
<213> Conus catus
<400> 338
Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe Asn Cys Cys 1 \hspace{1cm} 10 \hspace{1cm} 15
```

```
Ser Gly Ser Cys Asn Arg Gly Arg Cys
<210> 339
<211> 33
<212> PRT
<213> Conus caracteristicus
<400> 339
Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr
Pro
<210> 340
<211> 26
<212> PRT
<213> Conus consors
<400> 340
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
<210> 341
<211>
       25
<212> PRT
<213> Conus consors
<400> 341
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210> 342
<211> 36
<212> PRT
<213> Conus consors
<400> 342
Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met
1 10 15
Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn
Tyr Pro Gln Asn
<210> 343
<211>
       27
<212> PRT
<213> Conus catus
<400> 343
Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys
```

```
10
                                                         15
1
His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys
            20
<210> 344
<211> 25
<212> PRT
<213> Conus consors
<400> 344
Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
                                     10
Thr Gly Ser Cys Asn Arg Gly Lys Cys
<210> 345
<211> 26
<212> PRT
<213> Conus consors
<400> 345
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
<210> 346
<211> 25
<212> PRT
<213> Conus consors
<400> 346
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210> 347
<211> 35
<212> PRT
<213> Conus consors
<400> 347
Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe
Pro Ser Asn
<210> 348
<211> 25
<212> PRT
<213> Conus circumcisus
<400> 348
Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
```

```
Ser Gly Ser Cys Ser Asn Gly Arg Cys
            20
<210> 349
<211> 35
<212> PRT
<213> Conus circumcisus
<400> 349
Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
Thr Cys Cys Gly Tyr Cys Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe
                                25
Pro Ser Asn
        35
<210> 350
<211>
      27
<212> PRT
<213> Conus circumcisus
<400> 350
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
Ser Gly Ser Cys Ser Arg Tyr Ser Gly Arg Cys
<210> 351
<211> 35
<212> PRT
<213> Conus circumcisus
<400> 351
Ser Thr Gly Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr
Pro Ser Asn
<210> 352
<211> 28
<212> PRT
<213> Conus dalli
<400> 352
Ser Cys Thr Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys
Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu
<210> 353
<211> 25
<212> PRT
<213>
      Conus distans
<220>
<221> PEPTIDE
```

```
<222> (1)..(25)
<223> Xaa is Hyp
<400> 353
Cys Glu Asp Xaa Gly Glu Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
Gly Ser Cys Asn His Asn Val Cys Ala
<210>
      354
<211>
      27
<212> PRT
<213> Conus ermineus
<400> 354
Pro Cys Lys Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Pro
<210>
     355
<211> 27
<212> PRT
<213> Conus ermineus
<400> 355
Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
<210> 356
<211> 27
<212> PRT
<213> Conus geographus
<400> 356
Cys Lys Ser Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys
Arg Ser Cys Asn Pro Tyr Ala Lys Arg Cys Tyr
<210> 357
<211> 29
<212> PRT
<213> Conus geographus
<400> 357
Cys Lys Ser Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys
Thr Pro Cys Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
<210>
      358
<211>
       30
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
```

```
<400> 358
Cys Leu Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
Thr Ser Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys 20 25 30
<210>
      359
<211>
      27
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<400> 359
Cys Lys Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys
Ser Lys Phe Cys Asn Glu His Leu His Met Cys
<210>
       360
<211> 26
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<400> 360
Cys Lys Pro Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys
Asn Phe Cys Asn Thr His Leu Asn Met Cys
            20
<210> 361
<211> 28
<212> PRT
<213> Unknown
<220>
<223> unknown Conus species
<400> 361
Cys Ala Gly Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr
Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
            20
<210> 362
<211> 27
<212> PRT
<213> Conus laterculatus
<400> 362
Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
 Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Tyr
            20
```

```
<210> 363
<211> 27
<212> PRT
<213> Conus laterculatus
<400> 363
Cys Leu Pro Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys
Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser
<210> 364
<211> 30
<212> PRT
<213> Conus lynceus
<400> 364
Cys Lys Ser Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys
Thr Phe Cys Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
                                 25
<210> 365
<211> 28
<212> PRT
<213> Conus lynceus
<400> 365
Cys Ala Gly Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr
Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
                                 25
<210> 366
<211> 27
<212> PRT
<213> Conus lynceus
<400> 366
Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
<210> 367
<211> 27
<212> PRT
<213> Conus lynceus
Lys Cys Trp Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys
Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Tyr
<210> 368
<211> 29
<212> PRT
<213> Conus laterculatus
```

```
<400> 368
Cys Lys Ser Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
<210> 369
<211> 27
<212> PRT
<213> Conus laterculatus
<400> 369
Thr Cys Trp Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
             20
<210> 370
<211> 27
<212> PRT
<213> Conus laterculatus
<400> 370
Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
<210> 371
<211> 37
<212> PRT
<213> Conus leopardus
<400> 371
Ser Leu Phe Glu Cys Ala Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys
Ser Cys Cys Glu Gly Tyr Cys Asp Gly Glu Ser Thr Ser Cys Val Ser
Gly Pro Tyr Ser Ile
<210> 372
<211> 30
<212> PRT
<213> Conus leopardus
<400> 372
Trp Pro Leu Asp Cys Thr Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro
Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
                                 25
<210> 373
<211> 31
<212> PRT
<213> Conus leopardus
Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu
```

```
10
                                                         15
Ile Cys Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
                                 25
<210> 374
<211> 27
<212> PRT
<213> Conus leopardus
<400> 374
Tyr Cys Ala Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
Gly Tyr Cys Glu Thr Phe Tyr Asn Thr Cys Arg
<210> 375
<211> 25
<212> PRT
<213> Conus magus
<400> 375
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210> 376
<211> 26
<212> PRT
<213> Conus magus
<400> 376
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
                                                         15
Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
<210> 377
<211> 27
<212> PRT
<213> Conus miles
<400> 377
Cys Asn Asp Arg Gly Gly Cys Ser Gln His Pro His Cys Cys Gly
Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
            20
<210>
      378
<211>
       25
<212> PRT
<213> Conus monachus
<400> 378
Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
            20
```

```
<210> 379
 <211> 25
 <212> PRT
 <213> Conus monachus
 <400> 379
 Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys
 Thr Gly Ser Cys Asn Arg Gly Lys Cys
<210> 380
<211> 35
<212> PRT
<213> Conus obscurus
<400> 380
Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr
                                 25
Pro Gln Asn
        35
<210> 381
<211> 28
<212> PRT
<213> Conus obscurus
<400> 381
Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
                                    10
Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
<210> 382
<211> 27
<212> PRT
<213> Conus purpurascens
<220>
<221>
      PEPTIDE
<222>
       (1)..(27)
<223> Xaa is Hyp
<400> 382
Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
<210>
      383
<211>
      26
<212> PRT
<213> Conus purpurascens
<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 5 is Hyp; Xaa at residue 12 is gamma-carboxy-Glu
```

```
<400> 383
 Ser Cys Lys Leu Xaa Gly Ala Tyr Cys Asn Ala Xaa Asp Tyr Asp Cys
 Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
 <210> 384
 <211> 27
 <212> PRT
 <213> Conus purpurascens
 <400> 384
Pro Cys Lys Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
 Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
             2.0
 <210>
       385
 <211> 30
<212> PRT
<213> Conus pulicarius
<400> 385
Gln Cys Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
Ser Leu Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
<210> 386
<211> 27
<212> PRT
<213> Conus pulicarius
<400> 386
Glu Cys Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys
Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
<210> 387
<211> 27
<212> PRT
<213> Conus pulicarius
<400> 387
Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
                                    10
Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
<210>
       388
<211>
       28
<212> PRT
<213> Conus radiatus
<400> 388
His Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
                5
```

```
Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
 <210> 389
 <211>
        28
 <212>
       PRT
 <213> Conus radiatus
 <400> 389
 Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
 Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
 <210> 390
 <211> 27
 <212> PRT
 <213> Conus rattus
<400> 390
Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser
Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
            20
<210> 391
<211> 27
<212> PRT
<213> Conus rattus
<400> 391
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
                                    10
Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
<210> 392
<211> 27
<212> PRT
<213> Conus rattus
<400> 392
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
            20
                                25
<210> 393
<211> 34
<212> PRT
<213> Conus rattus
<400> 393
Ala Cys Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys
                                   10
Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser
Leu His
```

```
<210> 394
 <211> 36
<212> PRT
 <213> Conus striatus
 <400> 394
 Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met
 Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn
 Tyr Pro Lys Asn
         35
 <210> 395
 <211> 26
 <212> PRT
 <213> Conus striatus
<400> 395
Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr Asp Cys Cys
Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
<210> 396
<211> 25
<212> PRT
<213> Conus striatus
<400> 396
Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
Thr Gly Ser Cys Arg Ser Gly Lys Cys
<210> 397
<211> 26
<212> PRT
<213> Conus striatus
<400> 397
Cys Glu Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
Ala Cys Asp Pro Ala Lys Lys Thr Cys Thr
       398
<210>
<211>
       27
<212> PRT
<213> Conus stercusmuscarum
<400> 398
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
Ser Gly Ser Cys Ser Gly Tyr Thr Gly Arg Cys 20 25
```

```
<210> 399
 <211> 35
<212> PRT
 <213> Conus stercusmuscarum
 <400> 399
 Thr Thr Ser Cys Met Gln Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg
 Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr
 Pro Ser Asn
         35
<210> 400
<211> 26
<212> PRT
<213> Conus stercusmuscarum
<400> 400
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr
<210> 401
<211> 26
<212> PRT
<213> Conus stercusmuscarum
<400> 401
Cys Val Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
                                                          15
Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr
<210> 402
<211> 25
<212> PRT
<213> Conus stercusmuscarum
<400> 402
Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys
Ser Gly Ser Cys Thr Arg Gly Arg Cys
<210> 403
<211> 25
<212> PR
       PRT
<213> Conus striolatus
<400> 403
Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys
Thr Gly Ser Cys Asn Arg Gly Arg Cys
<210> 404
<211> 24
```

```
<212> PRT
 <213> Conus striolatus
<400> 404
Cys Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly
                                    10
Arg Cys Val Asn Arg Arg Cys Thr
<210> 405
<211> 35
<212> PRT
<213> Conus striolatus
<400> 405
Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg
Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr
Pro Lys Asn
   35
<210> 406
<211> 28
<212> PRT
<213> Conus textile
<400> 406
Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys
                                    10
Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
<210> 407
<211> 31
<212> PRT
<213> Conus viola
<400> 407
Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
<210> 408
<211> 25
<212> PRT
<213> Conus viola
<400> 408
Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
Thr Gly Ser Cys Arg Asn Gly Lys Cys
<210> 409
<211> 36
<212> PRT
<213> Conus viola
```

```
<400> 409
Ser Thr Ser Cys Met Glu Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr
Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
Asn Pro Asn Asn
       35
<210> 410
<211> 25
<212> PRT
<213> Conus viola
<400> 410
Cys Lys Gly Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys
                                    10
Lys Tyr Ser Cys Gly Asn Gly Lys Cys
<210> 411
<211>
<212>
       28
      PRT
<213> Conus viola
<400> 411
Tyr Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys
Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
            20
<210> 412
<211> 27
<212> PRT
<213> Conus textile
<400> 412
Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser
His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
<210> 413
<211> 26
<212> PRT
<213> Conus tulipa
<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa is Hyp
<400> 413
Cys Lys Ser Trp Gly Ser Xaa Cys Ser Xaa Thr Ser Thr Asn Cys Cys
Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys
```